

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THE FACE BLANK (USPTO)

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2003, 19:37:55 ; Search time 1730 Seconds
(without alignments)
8032.213 Million cell updates/sec

Title: US-10-031-403-2
Perfect score: 858
Sequence: 1 aatcccgatccctgcgcgc.....agactgcgcgattcccaaa 858

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 1
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estnu:*
4: em_estov:*
5: em_estpl:*
6: em_estro:*
7: em_esthc:*
8: em_estl:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: em_estfun:*
15: em_estom:*
16: em_gss:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	761.4	88.7	867	12	BG697492
2	750.8	87.5	819	12	BG680086
3	737.2	85.9	830	12	BG743203
4	715.4	83.4	976	12	BG676307
5	685.2	79.9	721	12	BG696865
6	500.8	58.4	508	9	AI791495

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT
BG697492	60260685F1	NCI CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4803932 5', mRNA sequence.	BG697492	BG697492.1	GI:13963770	EST.	human.	1	(bases 1 to 867)	NIH-MGC http://mgc.nci.nih.gov/.	Unpublished (1999)
BG697492	60260685F1	NCI CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4803932 5', mRNA sequence.	BG697492	BG697492.1	GI:13963770	EST.	human.	1	(bases 1 to 867)	NIH-MGC http://mgc.nci.nih.gov/.	Unpublished (1999)
BG697492	60260685F1	NCI CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4803932 5', mRNA sequence.	BG697492	BG697492.1	GI:13963770	EST.	human.	1	(bases 1 to 867)	NIH-MGC http://mgc.nci.nih.gov/.	Unpublished (1999)

ALIGNMENTS

AI732539	n101f09.x	AI791325	aes6g09.y	AA709067	zif6f02.s	AM082062	xb59g06.x	BG676779	602623367	AI791964	nn90g08.y	AA505923	n101f09.s	AI732667	nn90g08.x	AI909857	QV-BT225-	AI909862	QV-BT225-	AA601601	nn90g08.s	BG681217	602629361	AM057561	wy6g060.x	BE012482	121944.MA	AM464722	BP230016B	AI909853	QV-BT225-	AI787098	120812.MA	BG676223	602622621	BG695851	602657814	BG674179	602619819	BG740422	602633810	BG697978	602659118	BG743500	602635530	BE742955	602632055	BE583734	4-4B-HA.P	BE583164	1-12F-MY	BG696929	602703348	AV606393	AV606393	BO24580	TAE15017F	BO294870	WHE2855.D	BF259672	HVSMEF001	AK009664	Mus muscu	BO755173	EBe402.SQ	BO660636	H104K03u	BF259676	HVSMEF001	AV915211	AV915211	AV921849	AV921849	AL506588	AL506588	BF254128	HVSMEF000
----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	----------	----------	-----------	----------	----------	---------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	----------	----------	-----------	----------	----------	----------	----------	----------	----------	----------	-----------

FEATURES

Source

1. 867

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1AM10700 row: 1 column: 21 High quality sequence stop: 828. Location/Qualifiers

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4803932"
/lab_host="NCI CGAP Skn4"
/Note="Organ: skin; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      187 a      252 c      296 g      132 t
ORIGIN

```

```

Query Match      88.7%; Score 761.4; DB 12; Length 867;
Best Local Similarity 97.7%; Pred. No. 2.2e-136;
Matches 804; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

Cy 37 CACGAGCTCTGAGACACAGGTTGAGGCGCGTGGGAGCGAGTCCGCGAG 96
    |||||||
Db 1 CACGAGCTCTGAGACACAGGTTGAGGCGCGTGGGAGCGAGTCCGCGAG 60
    |||||||
Qy 97 GTGACGAGACGACGAGCATGGCCGCTGAGCTGACTCTGAGAGAGAGCCAGTACAAA 156
    |||||||
Db 61 GTGACGAGACGACGAGCATGGCCGCTGAGCTGACTCTGAGAGAGAGCCAGTACAAA 120
    |||||||
Qy 157 AGGCTTCTCCGCGGTTACACGATGGAACGACGACATCATGCTCCAGAGCTGGGCG 216
    |||||||
Db 121 AGGCTTCTCCGCGGTTACACGATGGAACGACGACATCATGCTCCAGAGCTGGGCG 180
    |||||||
Qy 217 CGGCGCTGAAGGCCACGGGCAAGAACTCTCTGAGAGCCAGCTAAGAACTCATCTCG 276
    |||||||
Db 181 CGGCGCTGAAGGCCACGGGCAAGAACTCTCTGAGAGCCAGCTAAGAACTCATCTCG 240
    |||||||
Qy 277 AGCTTGACAGCAGCGGCGGCAATCAGCTTCAGAGTTCCTGACGCGCGCAAGA 336
    |||||||
Db 241 AGCTTGACAGCAGCGGCGGCAATCAGCTTCAGAGTTCCTGACGCGCGCAAGA 300
    |||||||
Qy 337 AGGCGAGGCGCGGCTGAGAGACCTGAGAGTCCGCTCCGCGGCTTCAGCAGAGTGGCG 396
    |||||||
Db 301 AGGCGAGGCGCGGCTGAGAGACCTGAGAGTCCGCTCCGCGGCTTCAGCAGAGTGGCG 360
    |||||||
Qy 397 ACGGCCACATCACCCTGAGACGAGCTCAGCGGCGCATGGCGGCGTGGGCGAGCGCTGC 456
    |||||||
Db 361 ACGGCCACATCACCCTGAGACGAGCTCAGCGGCGCATGGCGGCGTGGGCGAGCGCTGC 420
    |||||||
Qy 457 CGCAGAGAGAGCTGACCCCATGATCCCGAGGCGGAGCTGAGACAGGAGCGGCGTGA 516
    |||||||
Db 421 CGCAGAGAGAGCTGACCCCATGATCCCGAGGCGGAGCTGAGACAGGAGCGGCGTGA 480
    |||||||
Qy 517 ACTAGAGAGAGTGGCGAGAGTGTGCGGCGAGAGTGAAGGCTCCCGGCTGTGTCCCT 576
    |||||||
Db 481 ACTAGAGAGAGTGGCGAGAGTGTGCGGCGAGAGTGAAGGCTCCCGGCTGTGTCCCT 540
    |||||||
Qy 577 GGCCTGCGCTGAGAGCTTCAAGGCGCACCGCGCTGCTGTCTTTTGTGAGGACTCTCG 636
    |||||||
Db 541 GGCCTGCGCTGAGAGCTTCAAGGCGCACCGCGCTGCTGTCTTTTGTGAGGACTCTCG 600
    |||||||
Qy 637 GCGAAACTGTGCTGAGTGGGAACTGCTCCCTCGGAGAGAGGCTTTGCGCTCG 696
    |||||||
Db 601 GCGAAACTGTGCTGAGTGGGAACTGCTCCCTCGGAGAGAGGCTTTGCGCTCG 660
    |||||||
Qy 697 GGGGCTGGA-TGGGCGCGCTCGGCGCGCTGCGAGCGCCCTCTGCTTGAAGACTTGG 755
    |||||||
Db 661 GGGGCTGAGTTGGCGCGCTCGGCGCGCTGCGAGCGCCCTCTGCTTGAAGACTTGG 720
    |||||||
Qy 756 GCAGAGAGAGCTTCTTGGGCTGTGTCCTCTTGGCTCCCTCAGTGAAGAGCGGCT 815
    |||||||
Db 721 GCAGAGAGAGG-CTCTCTTGGGCTGTGTCCTCTTGGCTCCCTCAGTGAAGAGG-CCCT 778
    |||||||
Qy 816 TTAACCCGCAATGATCTAATTAAGAGACTGCGAGTTCCAAA 858
    |||||||
Db 779 TCAGCCCGCAATGATCTAATTAAGAGATTCGAGTTCCAAA 821
    |||||||

```

```

RESULT 2
Bg680086
LOCUS
DEFINITION
Bg680086 819 bp mRNA linear EST 01-MAY-2001
602628238P1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4753280 5',
mRNA sequence.
ACCESSION
Bg680086
VERSION
Bg680086.1 GI:13911483
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 819)
Nih-MGC http://mgi.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
CONTACT
Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM10612 row: k column: 09
High quality sequence stop: 819.
Location/Qualifiers
1. 819
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4753280"
/tissue_type="squamous cell carcinoma"
/lab_host="NCI CGAP Skn4"
/Note="Organ: skin; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      139 a      256 c      300 g      124 t
ORIGIN

```

```

Query Match      87.5%; Score 750.8; DB 12; Length 819;
Best Local Similarity 96.6%; Pred. No. 2.4e-134;
Matches 799; Conservative 0; Mismatches 7; Indels 4; Gaps 4;

Qy 4 TCCCGATCCCTGCGCGCTGCTGACACACGAGCTCTGAGACAGGTTGAG 63
    |||||||
Db 7 TCCCGATCCCTGCGCGCTGCTGACACACGAGCTCTGAGACAGGTTGAG 66
    |||||||
Qy 64 GGCCTGAGGAGCAGCTGAGAGGCTCCGAGGTGACGAGACGAGCATGGCGGTG 123
    |||||||
Db 67 GGCCTGAGGAGCAGCTGAGAGGCTCCGAGGTGACGAGACGAGCATGGCGGTG 126
    |||||||
Qy 124 AGCTGACTCTGAGAGAGAGGCCAGTACAAAAGGCTTTCTCCGCGTGAACAGGATG 183
    |||||||
Db 127 AGCTGACTCTGAGAGAGAGGCCAGTACAAAAGGCTTTCTCCGCGTGAACAGGATG 186
    |||||||
Qy 184 GAAACGACACATCAATCCAGAGAGTGGCGCGCTGTAAGGCGACGGCAAGAAC 243
    |||||||
Db 187 GAAACGACACATCAATCCAGAGAGTGGCGCGCTGTAAGGCGACGGCAAGAAC 246
    |||||||
Qy 244 TCTCGAGAGCCAGCTAAGAACTCATCTCCGAGTTGACAGCGAGCGGCGAA 303
    |||||||
Db 247 TCTCGAGAGCCAGCTAAGAACTCATCTCCGAGTTGACAGCGAGCGGCGAA 306
    |||||||
Qy 304 TCAGCTTCAGAGAGTCTCTGACGCGGCGCAAGAGGCGCGGCTGAGAGACTGCG 363
    |||||||
Db 307 TCAGCTTCAGAGAGTCTCTGACGCGGCGCAAGAGGCGCGGCTGAGAGACTGCG 366
    |||||||
Qy 364 AGGTGCGCTTCCGCGCTTCGACCAAGATGGGAGCGGCACATCAGCTGAGAGCTCA 423
    |||||||
Db 367 AGGTGCGCTTCCGCGCTTCGACCAAGATGGGAGCGGCACATCAGCTGAGAGCTCA 426
    |||||||

```

QY 424 GCGGGCCATGGCGGGCTGGGGAGCCGCTGCCAGAGAGGCGGACGCCATGATCC 483
 DB 427 GCGGGCCATGGCGGGCTGGGGAGCCGCTGCCAGAGAGGCGGACGCCATGATCC 486
 QY 484 GCGAGCGCGACGTGAGACGAGAGCGGGGTGTAACCTACAGAGAGTTCGGAGAGTCTCG 543
 DB 487 GCGAGCGCGACGTGAGACGAGAGCGGGGTGTAACCTACAGAGAGTTCGGAGAGTCTCG 546
 QY 544 CCCAGAGAGTGAAGGCTCCCGCTGTGTCCCTGGCTGCGCTCTGAGCCTTACAGGCCAC 603
 DB 547 CCCAGAGAGTGAAGGCTCCCGCTGTGTCCCTGGCTGCGCTCTGAGCCTTACAGGCCAC 606
 QY 604 GCGCGCGCTGCTCTTTGTGTGTGGAGCTCCGGGAAACCTGCTGGGTGGATGGGAAAC 663
 DB 607 CG-CGCGTGTCTTTGTGTGTGGAGCTCCGGGAAACCTGCTGGGTGGATGGGAAAC 665
 QY 664 TGCCCTCCCGCTGGAGAGGCTTTCGCTCCGGGCGCTGATGCGGCGCCCTCGGGCCG 723
 DB 666 TGCCCTCCCGCTGGAGAGGCTTTCGCTCCGGGCGCTGATGCGGCGCCCTCGGGCCG 725
 QY 724 CCGGAGAGCCCTCTCTGCTCTGACACCTTGGGAGAGAGGCTCTTGGGCGCTGCTG 783
 DB 726 -CTGGAGCGCCCTCTCTG-CTCCAGACCTTGGGAGAGAGGCTCTTGGGCGCTGCTG 783
 QY 784 CCCCTTTGCCCTGACAGTGAATGAGGGCC 813
 DB 784 CCCCTTTG-CTGGAGTGAATGAGGGCC 812

RESULT 3
 LOCUS Bg743203 830 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602634365PL NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4779184 5',
 mRNA sequence.
 ACCESSION Bg743203
 VERSION Bg743203.1 GI:14053856
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 830)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Stransberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM10636 row: b column: 17
 High quality sequence stop: 823.
 Location/Qualifiers
 1. 830
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4779184"
 /clone_lib="NCI_CGAP_Skn3"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 139 a 257 c 303 g 131 t
 ORIGIN
 Query Match 85.9%; Score 737.2; DB 12; Length 830;
 Best Local Similarity 97.3%; Pred. No. 9,6e-132;

Matches 792; Conservative 0; Mismatches 18; Indels 4; Gaps 4;
 QY 3 TTCGGGATTCCTGGGGCTGCTGACATCTGGACACAGAGCTCTGAGACAGGATTA 62
 DB 10 TCCCGGATCCCTGGGGCTGCTGACATCTGGACACAGAGCTCTGAGACAGGATTA 69
 QY 63 GGGCGGTGGGAGGAGCTCGAGAGCTCCGAGAGTGCAGAGAGCCAGAGCTGGCGGT 122
 DB 70 GGGCGGTGGGAGGAGCTCGAGAGCTCCGAGAGTGCAGAGAGCCAGAGCTGGCGGT 129
 QY 123 GAGTGTACTCTGAGAGAGGAGCCAGTACAAAAGGCTTCTCCGGTTACACGGAT 182
 DB 130 GAGTGTACTCTGAGAGAGGAGCCAGTACAAAAGGCTTCTCCGGTTACACGGAT 189
 QY 183 GGAAGCGACATCAATATCCAGAGAGTGG-CCGCGGGCTTGAAGCCACAGGCAAGA 241
 DB 190 GGAAGCGACATCAATATCCAGAGAGTGGCGGGCGGGCTGAAGGCCACAGGCAAGA 249
 QY 242 CCTCTCGAGAGCCAGAGTAAAGAACTATCTCCGAGTTCAGACAGCGAGCGCA 301
 DB 250 CCTCTCGAGAGCCAGAGTAAAGAACTATCTCCGAGTTCAGACAGCGAGCGCA 309
 QY 302 AATCAGCTTCCAGAGATCTCTACGCGGCAAGAAAGCCAGAGCCGCTGAGAGACT 361
 DB 310 AATCAGCTTCCAGAGATCTCTACGCGGCAAGAAAGCCAGAGCCGCTGAGAGACT 369
 QY 362 GCAGGTGCGCTTCGCGGCTTTCGACAGAGTGGCGAGCCAGTACACCTGAGAGACT 421
 DB 370 GCAGGTGCGCTTCGCGGCTTTCGACAGAGTGGCGAGCCAGTACACCTGAGAGACT 429
 QY 422 CAGGCGGCGCATGGCGGCTGGGGAGCGCTGCGGAGAGAGTGGAGCCATGAT 481
 DB 430 CAGGCGGCGCATGGCGGCTGGGGAGCGCTGCGGAGAGAGTGGAGCCATGAT 489
 QY 482 CCGCGAGCGCGACGTRGACAGAGAGCGGGGTGAACACTACGAGAGTTCGCAAGATGCT 541
 DB 490 CCGCGAGCGCGACGTRGACAGAGAGCGGGGTGAACACTACGAGAGTTCGCAAGATGCT 549
 QY 542 GCGCCAGAGTGAAGGCTCCGCGCTGTGCTCCGCTGCGGCTGAGCTTCAGAGGCC 601
 DB 550 GCGCCAGAGTGAAGGCTCCGCGCTGTGCTCCGCTGCGGCTGAGCTTCAGAGGCC 608
 QY 602 ACCGCGCGCTGCTGCTTGTGCTGGAGCTTCGCGGAGAACTGCTGCGTGAATGGA 661
 DB 609 ACCGCGCGCTGCTGCTTGTGCTGGAGCTTCGCGGAGAACTGCTGCGTGAATGGA 668
 QY 662 ACTGCTCCCGC-TGGAGAGAGGCTTTCGCTCGGGGCTTGATGCGGCGCTCGGG 720
 DB 669 ACTGCTCCCGCCTTGGAGAGAGGCTTTCGCTCGGGGCTTGATGCGGCGCTCGGG 728
 QY 721 CCGCGTGGAGAGCCGCTGCTGCTTCAGACCTT-GGGAGAGAGAGGCTTCCTGGGCGT 779
 DB 729 CCGCGTGGAGAGCCGCTGCTGCTTCAGACCTTGGGAGAGAGGCTTCCTGGGCGT 788
 QY 780 GGTCCCGCTTTCGCTGACAGTGAATGAGGGCC 813
 DB 789 GGTCCCGCTTTCGCTGACAGTGAATGAGGGCC 822

RESULT 4
 LOCUS Bg676307 976 bp mRNA linear EST 01-MAY-2001
 DEFINITION 602622717PL NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4747661 5',
 mRNA sequence.
 ACCESSION Bg676307
 VERSION Bg676307.1 GI:13907703
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 976)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

LOCUS A1732539 508 bp mRNA linear EST 13-DEC-1999
 DEFINITION n101f09.x5 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966761 3'
 similar to SW:CALM_METSE P02596 CALMODULIN.; mRNA sequence.
 ACCESSION A1732539
 VERSION A1732539.1 GI:5053652
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 508)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bdrrp/image/image.html
 This read is a RESSEQUENCE of a previously sequenced human clone
 Original clone citation: National Cancer Institute, Cancer Genome
 Anatomy Project (CGAP), Tumor Gene Index
 This read has been verified (found to hit its original self in the
 correct orientation)
 Insert length: 936 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 464.
 Location/Qualifiers
 1. 508
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:966761"
 /clone_1id="NCI_CGAP_Br2"
 /sex="Female, pooled"
 /tissue_type="breast"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. 1st strand cDNA was prepared from pooled bulk
 breast tumor tissue, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT73
 vector. This library is the normalized version of
 NCI CGAP Br1.1. Library was constructed by Bento Soares
 and M. Fatima Bonaldo."
 BASE COUNT 87 a 177 c 166 g 78 t
 ORIGIN
 Query Match 58.3%; Score 500; DB 9; Length 508;
 Best Local Similarity 99.0%; Pred. No. 2.9e-86;
 Matches 503; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 351 CTGAGAGACTGTCAGGTCCTTCGGCCTTCGACGAGATGGCGAGCCACATCACC 410
 |||||||
 DB 508 CTGAGAGACCTGACGTCCTTCGGCCTTCGACGAGATGGCGAGCCACATCACC 449
 |||||||
 QY 411 GTGACGAGCTCAGCGCGGCATGGCGGCTGGGGCAGCCCTGCGCAGAGAGAGCTG 470
 |||||||
 DB 448 GTGACGAGCTCAGCGCGGCATGGCGGCTGGGGCAGCCCTGCGCAGAGAGAGCTG 389
 |||||||
 QY 471 GACCCATGATCCCGAGAGCGGAGCTGACGACGAGCGGCGGTGAATACGAGAGATTC 530
 |||||||
 DB 388 GACCCATGATCCCGAGAGCGGAGCTGACGACGAGCGGCGGTGAATACGAGAGATTC 329
 |||||||
 QY 531 GCGAGATGCTGCGCCAGAGAGTGAAGCTCCCGCCTGTGTCCCTGGCTGCTGAG 590
 |||||||

DB 328 GCGAGATGCTGCGCCAGAGAGTGAAGCTCCCGCTGTGTCCCTCGGCTGCTTTGAG 269
 QY 591 CTTTCAGGGCCACCGCCGCTGCTCTTTGTGTGGAGACTCTCCGGGAAACCTGTGCG 650
 |||||||
 DB 268 CTTTCAGGGCCACCGCCGCTGCTCTTTGTGTGGAGACTCTCCGGGAAACCTGTGCG 209
 |||||||
 QY 651 GTGATGGGAAACTGCTCCCTCCCTGGAGAGAGGCTTTGCGCTCGGGGCTGATGCGG 710
 |||||||
 DB 208 GTGATGGGAAACTGCTCCCTCCCTGGAGAGAGGCTTTGCGCTCGGGGCTGATGCGG 149
 |||||||
 QY 711 GCGCCGCGGCGCCTGAGAGCCCTCTCTGCTTCACACCTTGGGCAAGAGAGCCCTC 770
 |||||||
 DB 148 GCGCCGCGGCGCCTGAGAGCCCTCTCTGCTTCACACCTTGGGCAAGAGAGCCCTC 89
 |||||||
 QY 771 CTTGGGCTGTGCTCCCTCTTTCCTGACAGTGAATGAGAGCCCTTAACCCGATGAT 830
 |||||||
 DB 88 CTTGGGCTGTGCTCCCTCTTTCCTGACAGTGAATGAGAGCCCTTAACCCGATGAT 29
 |||||||
 QY 831 CTAATTAAGAGACTGCGAGTTCCAAA 858
 |||||||
 DB 28 CTAATTAAGAGACTGCGAGTTCCAAA 1
 |||||||
 RESULT 8
 A1791325
 LOCUS A1791325 508 bp mRNA linear EST 24-OCT-2000
 DEFINITION ae56g09.y5 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone
 IMAGE:950944 5' similar to SW:CALM_PLAFA P24044 CALMODULIN.; mRNA
 sequence.
 ACCESSION A1791325
 VERSION A1791325.1 GI:5339041
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 508)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Other ESTs: ae56g09.x5
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (infoimage.lnl.gov) for further information.
 This read is a RESSEQUENCE of a previously sequenced human clone
 Original clone citation: see original entry for original citation
 information
 This 5' ressequenced clone has no previous 5' data to verify this
 new read against
 Insert length: 587 Std Error: 0.00
 Seq primer: -40RP from Gibco
 High quality sequence stop: 486.
 Location/Qualifiers
 1. 508
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:950944"
 /clone_1id="Stratagene lung carcinoma 937218"
 /tissue_type="lung carcinoma"
 /cell_line="NCI-H69"
 /dev_stage="cell line NCI-H69"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: lung; Vector: pBluescript SK-; Site 1: EcoRI
 ; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
 dr. Small cell carcinoma cell line NCI-H69. Average
 insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
 sequence: 5' GAATTCGCGAGG 3' -3' adaptor sequence: 5'
 CTCGAGCTTTTCTTTTCTTTT 3'."
 BASE COUNT 100 a 153 c 189 g 65 t 1 others
 ORIGIN

Query Match	58.2%	Score 499.2	DB 9	Length 508
Best Local Similarity	99.2%	Pred. No. 4.1e-86		
Matches 501	Conservative 0	Mismatches 4	Indels 0	Gaps 0
OY	3	TTCCCGATCCCTGCGGCTGCTGCACCTGTGGACCCAGAGCTCTTGAGAGACAGCAGTTGA	62	
Db	4	TCGCCGATTCCTCGGGCTGCTGCACCTGTGGACCCAGAGCTCTTGAGAGACAGCAGTTGA	63	
OY	63	GGGCGCGTGGGAGAGAGCTCGAGGCTCCCGAGAGTGCAGAGACAGCAGGCTGCGGCT	122	
Db	64	GGGCGCGTGGGAGAGAGCTCGAGGCTCCCGAGAGTGCAGAGACAGCAGGCTGCGGCT	123	
OY	123	GAGCTACTCTCGAGAGAGAGCCACATCAAAAAAGGCTTTCTCCGCGGTTGACAGGAT	182	
Db	124	GAGCTACTCTCGAGAGAGAGCCACATCAAAAAAGGCTTTCTCCGCGGTTGACAGGAT	183	
OY	183	GGAAGCGGACCATATATGCCAGAGAGTGGGCGGCTGAAAGCCACCGGCAAGAAC	243	
Db	184	GGAAGCGGACCATATATGCCAGAGAGTGGGCGGCTGAAAGCCACCGGCAAGAAC	243	
OY	243	CTCTGGAGAGCCACCTAAGGAAATCATCTCCAGGTGAGACAGGAGCGGAGCGGAA	302	
Db	244	CTCTGGAGAGCCACCTAAGGAAATCATCTCCAGGTGAGACAGGAGCGGAGCGGAA	303	
OY	303	ATCAGCTTCAGAGATTCTCTGACGGCGCAAGAAAGCCAGGCGGCTGAGAGACCTG	362	
Db	304	ATCAGCTTCAGAGATTCTCTGACGGCGCAAGAAAGCCAGGCGGCTGAGAGACCTG	363	
OY	363	CAGGTGCGCTTCGCGGCTTCGACAGAGATGGCGGCGCATATCAGCTGAGACAGCTC	422	
Db	364	CAGGTGCGCTTCGCGGCTTCGACAGAGATGGCGGCGCATATCAGCTGAGACAGCTC	423	
OY	423	AGCGCGCCATGGCGGCGTGGGCGAGCCGCTGCGCGCAGAGAGAGCTGAGCCATGATC	482	
Db	424	AGCGCGCCATGGCGGCGTGGGCGAGCCGCTGCGCGCAGAGAGAGCTGAGCCATGATC	483	
OY	483	CGCGAGCGCGAGCTGGACAGGAGC 507		
Db	484	CGCGAGCGCGAGCTGGACAGGAGC 508		

RESULT 9
AA709067/c

LOCUS
DEFINITION
IMAGE:384795 3' similar to SW:CALM.CHLRE P04352 CALMODULIN. ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 488)
Hillier, L., Allen, M., Boyles, L., Dubuque, T., Geisel, G., Jost, S.,
Kizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,
J., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@imgdb.llnl.gov) for further information.
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 321.
Location/Qualifiers

Source	1.. 488
organism="Homo sapiens"	
/db_xref="GDB:1293053"	
/db_xref="taxon:9606"	
/clone="IMAGE:384795"	
/clone_id="Scores_fetal_heart_NbNhl9w"	
/sex="unknown"	
/dev_stage="19 weeks"	
/lab_host="DH10B (ampicillin resistant)"	
/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGACATGAGGAGCGCGCCGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Scores fetal lung NbNhl9w."	
BASE COUNT	85 a 166 c 162 g 75 t
ORIGIN	
Query Match	52.4%; Score 450; DB 9; Length 488;
Best Local Similarity	97.6%; Pred. No. 1.le-76;
Matches 478; Conservative	0; Mismatches 10; Indels 2; Gaps 2;
QY	369 GCCTTCGCGCGCTTGGACAGAGTGGCGACGCGCCATCACCCGTGACAGACTCAGCGG 428
Db	488 GCTTTTCGCGCGCTTGGACAGAGTGGCGACGCGCCATCACCCGTGACAGACTCAGCGG 429
QY	429 GCCATGCGCGGCGCTGGCGACGCGCGTGGCGGACGAGAGAGTGGACGCCATGTCGCGGAG 488
Db	428 GCCATGCGCGGCGCTGGCGACGCGCGTGGCGGACGAGAGAGTGGACGCCATGATCGCGGAG 369
QY	489 GCCGACGTGAGACAGAGAGCGCGGCGGTAACTACAGAGAGTGGCGGAGATGCTGCGCCAG 548
Db	368 GCCGACGTGAGACAGAGAGCGCGGCGGTAACTACAGAGAGTGGCGGAGATGCTGCGCCAG 309
QY	549 GAGTAGAGCGTCCCGCGTGTGCCCCCGGGCGGCGCTTGAGGCGTTCAAGGGCGACCGGCC 608
Db	308 GAGTGA-GCTCCCGCGCTGTGTGCCCTTCGCGTGTGAGCTTTTAAAGCCACCGGCC 250
QY	609 GCTGTGCTTTTGTGCTGGAGACTCCGCGGGAACCTGATGCGATGGGAAATCTGCT 668
Db	249 GCTGTGCTTTTGTGCTGGAGACTCCGCGGGAACCTGATGCGATGGGAAATCTGCT 190
QY	669 CCCCCCTGGGAGAGAGGCTTTTGCGCTCGCGGGCGCTGGATGCGGGCGCCCTCGCTGC 728
Db	189 CCCCCCTGGGAGAGAGGCTTTTGCGCTCGCGGGCGCTGGATGCGCGGCCCTCGCTGC 131
QY	729 GAGCCCTCTCTGCTTGAGACCTTGGGCGAGAAAGAGGCGCTCTTGGGCGCTGATCCCTCT 788
Db	130 GAGCCCTCTCTGCTTGAGACCTTGGGCGAGAAAGAGGCGCTCTTGGGCGCTGATCCCTCT 71
QY	789 TTGCGCTCAGTGTAGTAGAGGGCCCTTAAACCCGCAATTGATCTAAATAAAGACTGCGG 848
Db	70 TTGCGCTCAGTGTAGTAGAGGGCCCTTAAACCCGCAATTGATCTAAATAAAGACTGCGG 11
QY	849 AGTTCCAAA 858
Db	10 AGTTCCAAA 1
RESULT 10	
LOCUS AM082062/c	483 bp mRNA linear EST 14-OCT-1999
DEFINITION	xb599g6.x1 NCI-GAP_Eso2 Homo sapiens cDNA clone IMAGE:2580634 3'
ACCESSION	AM082062
KEYWORDS	AM082062.1 GI:6037214
EST.	

QY	559	CCCCCGCTGATC--CCCGTGGCTGGCTGAGCCCTTCAAGGGCA--CGCCCGCTGCTG	61.5
Db	421	CCCCCGCTGTCTCTCCCTGTGCTTGGCTCTGAGCCCTTCAAGGGCAATCCCTGCTG	48.0
QY	616	CTTTTGTGCTGGGACTCTCCGGGGAAACCTGATGGTGG--ATGGGAACATGCCGCCCT	67.4
Db	481	CTTTTGTGCTGGGACTCTCCGGGGAAACCTGATGGTGGCATGGGAACCTGCTCCCT	54.0
QY	675	GGG-AGGAAGCTTTTGGGCTCCGGGGCTGGATGCGGCGCTTCGGCG--CCTGGAG	73.1
Db	541	GGGAGGAAGCTTTTGGGCTCCGGGGCTGGATGCGGCGCTTCGGCGCTTTGGAG	60.0
QY	732	CCCCCTCTGCTTC-AGACCTTGGGAGAAGAGGCTCTCTTGGGCTGTGCCCTTT	79.0
Db	601	CCCCCTCTGCTTCCTGAGACCTTGGGAGAAGAGGCTCTCTTGGGCTGTGCCCTTT	66.0
QY	791	GCCCGAGTGAATGAGGGCCCTTAACCCCGATTGATCTAAT--AAAGACTGCC	84.8
Db	661	GCCCGAGTGAATGAGGGCCCTTAACCCCGATTGATCTAATTAAGAGACTGCC	72.0
QY	849	AGTTCAAA 858 	
Db	721	AGTTCCAA 730	

```

/clone="IMAGE:966761"
/clone_lib="NCI_CGAP_Br2"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. This library is the normalized version of
NCI_CGAP_Br1.1. Library was constructed by Bento Soares
and M. Fatima Bonaldo."
BASE COUNT      68 a      124 c      121 g      61 t
ORIGIN

```

Query Match 37.9%; Score 325.4; DB 9; Length 374;

Best Local Similarity 95.2%; Pred. No. 8.5e-53; Mismatches 16; Indels 2; Gaps 2;

```

Matches 357; Conservative 0; Mismatches 16; Indels 2; Gaps 2;
QY 483 CGGAGGCGGACGTGACGACGAGGCGGGGTGACGAGGAGTTCGGAGGATGCTC 542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 374 CGGAGGCGGACGTGACGACGAGGCGGGGTGACGAGGAGTTCGGAGGATGCTC 315
QY 543 GCGGAGAGTGAAGGCTCCCGGCTGTGTCCCGCTGCGCTGTGAGCTTCAGGGCCA 602
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 314 GCGGAGAGTGAAGGCTCCCGGCTGTGTCCCGCTGCGCTGTGAGCTTCAGGGCCA 255
QY 603 CCGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 662
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 254 CCGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 195
QY 663 CT-GCCTCCCGCTGAGAGAGGCTTTCGCTCCGGGCGCTGATGCGCGCCCTCGGCG 721
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 194 CTGAGACTCCCGCTGAGAGAGGCTTTCGCTCCGGGCGCTGATGCGCGCCCTCGGCG 136
QY 722 CGGCTGAGAGGCTTTCGCTCCCGCTGAGAGGCTTTCGCTCCGGGCGCTGATGCGCG 781
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 135 CGGCTGAGAGGCTTTCGCTCCCGCTGAGAGGCTTTCGCTCCGGGCGCTGATGCGCG 76
QY 782 TCCGCTGAGAGGCTTTCGCTCCCGCTGAGAGGCTTTCGCTCCGGGCGCTGATGCGCG 841
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 75 TCCGCTGAGAGGCTTTCGCTCCCGCTGAGAGGCTTTCGCTCCGGGCGCTGATGCGCG 16
QY 842 ACTGCGGAGTTCCA 856
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 15 ACTGCGGAGTTCCA 1

```

```

RESULT 14      323 bp      mRNA      linear      EST 13-DEC-1999
A1732667/c    nm90808.x5 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1098494.3'
LOCUS          mRNA sequence.
DEFINITION
ACCESSION      A1732667
VERSION        A1732667.1 GI:5053780
KEYWORDS
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE      1 (bases 1 to 323)
AUTHORS       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE         National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL       Tumor Gene Index
COMMENT       Unpublished (1997)
                Contact: Robert Strausberg, Ph.D.
                Email: cga@bbs.femail.nih.gov
                Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                Emmert-Buck, M.D., Ph.D.
                CDNA Library Preparation: M. Bento Soares, Ph.D.
                CDNA Library Arrayed by: Greg Lennon, Ph.D.

```

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

This read is a RESSEQUENCE of a previously sequenced human clone
 Original clone citation: National Cancer Institute, Cancer Genome
 Anatomy Project (CGAP), Tumor Gene Index
 This read has been verified (found to hit its original self in the
 correct orientation)
 Insert length: 418 Std Error: 0.00
 Seq primer: -400P from Glibco.

```

FEATURES
    source
        location/Qualifiers
            1..323
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:1098494"
                /clone_lib="NCI_CGAP_Br2"
                /sex="female, pooled"
                /tissue_type="breast"
                /lab_host="DH10B"
                /note="Vector: pT73D-Pac (Pharmacia) with a modified
                polylinker; 1st strand cDNA was prepared from pooled bulk
                breast tumor tissue, and was then primed with a Not I -
                oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                RI adaptors (Pharmacia), digested with Not I and cloned
                into the Not I and Eco RI sites of the modified pT73
                vector. This library is the normalized version of
                NCI_CGAP_Br1.1. Library was constructed by Bento Soares
                and M. Fatima Bonaldo."

```

```

BASE COUNT      64 a      103 c      111 g      45 t
ORIGIN

```

Query Match 36.7%; Score 315; DB 9; Length 323;

Best Local Similarity 98.5%; Pred. No. 8.4e-51; Mismatches 5; Indels 0; Gaps 0;

```

Matches 318; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 533 GAGATGCTGCGCCGAGAGTGAAGGCTCCCGCTGTGTCCCGCTGCGCTGTGAGCC 592
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 323 GAGATGCTGCGCCGAGAGTGAAGGCTCCCGCTGTGTCCCGCTGCGCTGTGAGCC 264
QY 593 TTCAAGGCGCACCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 652
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 263 TTCAAGGCGCACCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 204
QY 653 GGATGGGAAACTGCTCCCTCGGAGAGAGGCTTTCGCTCCGGGCGCTGATGCGCG 712
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 203 GGATGGGAAACTGCTCCCTCGGAGAGAGGCTTTCGCTCCGGGCGCTGATGCGCG 144
QY 713 CCTCGGCGCGCTGCGAGCCCTCTGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 772
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 143 CCTCGGCGCGCTGCGAGCCCTCTGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 84
QY 773 TGGGCGCTGTCCTCCCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCG 832
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 83 TGGGCGCTGTCCTCCCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCG 24
QY 833 AAATGAAGGACTGCGGAGTTCCA 855
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 23 AAATGAAGGACTGCGGAGTTCCA 1

```

```

RESULT 15      322 bp      mRNA      linear      EST 30-MAR-2000
A1909857/c    A1909857
LOCUS          mRNA sequence.
DEFINITION    OY-BR225-050599-063 BR225 Homo sapiens cDNA, mRNA sequence.
ACCESSION      A1909857
VERSION        A1909857.1 GI:6500537
KEYWORDS
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

REFERENCE
AUTHORS

1 (bases 1 to 322)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., de Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNAL
MEDLINE

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/seq/gethtml.pl?tl=QVst2-QV-BT225-063.html
 st3-05059864-1)

FEATURES

source

1..322
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="BT225"
 /sex="female"
 /dev_stage="Adult"
 /note="Organ: breast; Vector: puc18; Site: 1; Smat: Site: 2;
 Smat: A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No. 196
 716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

Seq primer: puc 18 forward.
 Location/Qualifiers

BASE COUNT 64 a 106 c 107 g 45 t
 ORIGIN

Query Match

34.2%; Score 293.2; DB 9; Length 322;
 Best Local Similarity 94.4%; Pred. No. 1.3e-46;

Matches 304; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```

QY 490 CCGAGCTGGACGACGAGCGGGGCTGAGTACGAGAGGAGTTCGGAGAGTCTGCCAGG 549
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 322 CCAAGCTGACACAGACGAGCGGGGTGACCTACGAGAGTTCGCGAGATGCTGCCAGA 263

QY 550 AGTGAGCTCCCGCGCTGTGTCCCTGGCTGGCTCTGAGCCTCAGGGCCACGCCCG 609
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 262 AGTGAGCTCCCGCGCTGTGTCCCTGGCTGGCTCTGAGCCTCAGGGCCACGCCCG 203

QY 610 CTGCTGCTTTTGTGCTGGGACTCTCCGGGAAACCTGTGTGGATGGGAAACTGCCTC 669
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 202 TTGCTGCTTTTGTGCTGGGACTCTCCGGGAAACCTGTGTGGATGGGAAACTGCCTC 143

QY 670 CCCCTGGAGGAAGCTTTCGCGCTCCGGGGCTGGATGGGGCGCCCTCGGGCGCTGCG 729
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 142 CCCCTGGAGGAAGCTTTCGCGCTCCGGGGCTGGATGGGGCGCCCTCGGGCGCTGCG 83

QY 730 AGCCCTCTCTGCTTCAGACCTTGGGCAAGAGAGCCCTCTTGGGCTGTGCCCTT 789
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 82 AGCCCTCTCTGCTTCAGACCTTGGGCAAGAGAGCCCTCTTGGGCTGTGCCCTT 23

QY 790 TGGCTGCACTGATGAGGCG 811
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 22 TGGCTGCACTGATGAGGCG 1

```

Search completed: May 16, 2003, 01:11:33
 Job time : 1740 secs

Best Local Similarity 99.1%; Pred. NO. 1.7e-149;
Matches 837; Conservative 0; Mismatches 6; Indels 2;
Gaps 2

```

QY 3 TTCCCGATCCCTGGGCTGCTGACCTTGAGACCAAGCCTTGAGACCAAGCTTGA 62
Db 10 TGCCCGATCCCTGGGCTGCTGACCTTGAGACCAAGCCTTGAGACCAAGCTTGA 69
QY 63 GGGCCGATGGGAGCAGCTCGAGAGCTCCGAGAGTGCAGAGAGCAGCATGGCCGT 122
Db 70 GGGCCGATGGGAGCAGCTCGAGAGCTCCGAGAGTGCAGAGAGCAGCATGGCCGT 129
QY 123 GAGCTGATCTCTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 182
Db 130 GAGCTGATCTCTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 189
QY 183 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 242
Db 190 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 249
QY 243 CTCTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 302
Db 250 CTCTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 309
QY 303 ATCAGCTTCCAGAGAGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 362
Db 310 ATCAGCTTCCAGAGAGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 369
QY 363 CAGGTCGCTTCCGAGGAGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 422
Db 370 CAGGTCGCTTCCGAGGAGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 429
QY 423 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 482
Db 430 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 489
QY 483 GCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 542
Db 490 GCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 549
QY 543 GCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 602
Db 550 GCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 608
QY 603 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 662
Db 609 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 668
QY 663 CTGCTCTCCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 722
Db 669 CTGCTCTCCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 728
QY 723 GCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 782
Db 729 GCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 788
QY 783 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 842
Db 789 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 847
QY 843 CTGCG 847
Db 848 CTGCG 852

```

```

RESULT 2
US-09-285-601-1
; Sequence 1, Application us/09285601
; Patent No. 6248528
; GENERAL INFORMATION:
; APPLICANT: Chen, Hong
; APPLICANT: Freilmer, Nelson
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
; FILE REFERENCE: 7853-089
; CURRENT APPLICATION NUMBER: US/09/285, 601
; CURRENT FILING DATE: 1999-04-02

```

```

; EARLIER APPLICATION NUMBER: 60/080, 841
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)..(564)
US-09-285-601-1

```

```

Query Match 14.4%; Score 123.4; DB 4; Length 1173;
Best Local Similarity 57.6%; Pred. No. 6.1e-16;
Matches 245; Conservative 0; Mismatches 171; Indels 9; Gaps 1;

```

```

QY 123 GAGCTGATCTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 182
Db 118 GAGCTGATCTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 177
QY 183 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 242
Db 178 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 237
QY 243 CTCTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 302
Db 238 CCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 297
QY 303 ATCAGCTTCCAGAGAGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 362
Db 298 ATCAGCTTCCAGAGAGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 357
QY 354 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 413
Db 358 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 417
QY 414 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 473
Db 418 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 477
QY 474 GCGATGATCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 533
Db 478 GAGATGATCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 537
QY 534 AGGAT 538
Db 538 CGGAT 542

```

```

RESULT 3
US-09-285-601-3
; Sequence 3, Application us/09285601
; Patent No. 6248528
; GENERAL INFORMATION:
; APPLICANT: Chen, Hong
; APPLICANT: Freilmer, Nelson
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
; FILE REFERENCE: 7853-089
; CURRENT APPLICATION NUMBER: US/09/285, 601
; EARLIER FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: 60/080, 841
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-285-601-3

```

```

Query Match 14.4%; Score 123.4; DB 4; Length 6709;

```


Best Local Similarity 57.6%; Pred. No. 7e-16;
Matches 245; Conservative 0; Mismatches 171; Indels 9; Gaps 1;

```

QY 123 GAGCTGACCTCCGAGAGAGGCGCCAGTACAAAAGGCTTTCGCCGGTTCGACAGGAT 182
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3015 GAGCTCAGTACGAGATCAGAAAGAAAGTTGGGGAAGACATTCCTTCGACGTGGAC 3074
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 183 GGAACGCGCCATCATATGCCAGAGCTGGCGCGCTGAAAGCCACGGGCAAGAAC 242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3075 GGAAGTGGAGCATCGACGCGAAGAGCTGAAGTGGCCATGAGACCGCTGGCTTCGAA 3134
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 243 CTCTGGAGCGCCAGCTAAGAACTCATCTCCGAGGTTCGACGCGACGCGCGGAA 302
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3135 CCCAGAGAACGAGATGAAAGAAATGATCTCCGAGGTGACAGGAGGACGCGGGAAG 3194
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 303 ATCAGCTTCAGAGATCTCGACGCGCGGCGAAGAG-----GCCAGGCGCGGCTTG 353
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3195 ATCAGCTTCATATGACTCTCTGCGCTGATGACGCGAAGATGTCGCAAGAAAGACACAAA 3254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 354 GAGGACCTGACAGGTGCGCTTCGCGCGCTTCGACAGATGCGCGACGCGCATCACCGTG 413
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3255 GAAGAAATCTGTAAGGCTTCAGGCGCTTTGATGACGATGAGACCGGAAAGATCTCGTTC 3314
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 414 GACGAGCTAGCGCGGCGCATGGCGGGCTGGGCGACCGCTGCGCGAAGAGAGCTGGAC 473
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3315 AAAAACCTGAAGCGTGTGCGCAACGAGCTGGGGGAGAACCTCAGCGATGAGAGCTGCAG 3374
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 474 GCGATCTGCGGAGGCGAGCGACGCTGAGCAAGAGCGGGGGTGGTACGAGAGGCTTCGG 533
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3375 GAGATGATGACGAGACGATGATGCGGATGGGAGCGCGAAGTGAACGAGGAGTTCCTT 3434
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 534 AGGAT 538
    |||||
DB 3435 CGGAT 3439
    |||||

```

RESULT 4 US-08-818-253-1

; Sequence 1, Application US/08818253
; Patent No. 5998204

GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,253
FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/043001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1929 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1926
US-08-818-253-1

Query Match 14.3%; Score 122.6; DB 2; Length 1929;
Best Local Similarity 56.0%; Pred. No. 9e-16;
Matches 258; Conservative 0; Mismatches 194; Indels 9; Gaps 1;

```

QY 105 GACGAGGATGCGCGGTGAGTCTGACCTGAGAGAGAGCCGACGAAAGAGGCTTTC 164
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 679 GCCCGCCGATGATACCACTGACAGAGACCAATTCAGAGTTCAAGAAAGCTTTC 738
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 165 TCCGCGGTTCACAGATGGAACGGCACCATCATATGCCAGAGAGCTGGCGCGGCTG 224
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 739 TCATTAATTCAGAAAGATGGGAGCGCACCATCACCACAAAGAACTTGGCACGTTATG 798
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 225 AAGGCCACGGGCAAGAACTCTCGAGAGCGCCAGCTAAGAACTCATCTCCGAGTTGAC 284
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 799 AGGTCCCTTGACCAAAACCAACGAGAGAAATTCAGAGATGATGATCAATGAAGTCGAT 858
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 285 AGCGAGCGGAGCGGCAAAATCACCTTCAGAGATTCCTGACGGCG-----GCAAG 335
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 859 GCTGATGGCATGGAACGATTTCTTCTGAAATTTCTTACTATGATGGCTACAAAAATG 918
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 336 AAGGCCAGGCGCGGCTGAGAGCTGCAAGTGGCTTCGCGCGCTTCGACCAAGATGGC 395
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 919 AAGGACACAGACAGCAAGAGAAATCCGAGAAAGCATTCGCTTTTTCAGAAAGATGG 978
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 396 GAGCGCCATCATCCGTGACAGAGCTCAGCGCGGCGCATGGCGGCGCTGGGCGACCGCTG 455
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 979 AACGGCTACATGACGCTGCTGTAATTACGTACAGTATGACAAACCTCGGGGGAAGTTA 1038
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 456 CCCGAGAGAGCTGAGCGCATGATCCGAGCGCGAGCTGAGCAAGAGCGGCGGCTG 515
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1039 ACAGATGAAGATTTATGAATGATGAAGGAAGCAAGATTCATGATGATGATGATGATG 1098
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 516 AACTACAGAGAGTTCCGAGAGAGCTCGCCGACAGAGTGAGG 556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1099 AACTATGAAGAGTTGTACAAATGATGACAGCAAGAGGGGG 1139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 5 US-08-818-253-5

; Sequence 5, Application US/08818253
; Patent No. 5998204

GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,253
FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:

```

: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Halle, Ph.D., Lisa A.
: REGISTRATION NUMBER: 38,347
: REFERENCE/DOCKET NUMBER: 07257/043001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619/678-5070
: TELEFAX: 619/678-5099
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1929 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: Coding Sequence
: LOCATION: 1...1926
: US-08-818-253-5

```

```

Query Match      14.3%; Score 122.6; DB 2; Length 1929;
Best Local Similarity 56.0%; Pred. No. 9e-16;
Matches 258; Conservative 0; Mismatches 194; Indels 9; Gaps 1;

```

```

QY 105 GAGCAGGATGCGCGGTGAGCTGCTCTGAGAGAGAGCCCACTACAAAGGCTTTC 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 679 GCCCGCCGATGATGACCAACTGACAGAGAGATTCGAGATTCAGAAAGCCCTTC 738
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 165 TCCCGGTTGACAGGATGGAAGGCGACATCAATGCCAGAGAGCTGGGCGCGCTG 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 739 TCATTATTCGACAGATGGGAGCGGACCATCCACCAAGAACTTGGACCGTTATG 798
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 225 AAGCCAGGCGCAAGAACTCTCGAGGCGCAGCTAAGAACTCATCTCCGAGTTGAC 284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 799 AGTCGCTTGACAAACCCCAAGCAAGCAATTCGAGATGATGATCAATGAAGTCAT 858
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 285 AGCGAGCGCGGCGGAATAGCTTCAGAGATTCCTGAGCGG-----GCAAG 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 859 GCTATGCAATGGAACGATTACTTCTGTAATTTCTTACTATGATGGCTAGAAAATG 918
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 336 AAGCCAGGCGCGCGCTGAGAGACCTGCGAGCTGCTCCGCGCTTCGACAGATGAC 395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 919 AAGGACACAGACAGCAAGAGAAATCCGAGAACATTCCTGTTTGGACAAAGATGG 978
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 396 GACGCGCATCATCCGTGAGAGAGCTCAGCGGCGCATGGCGGCGTGGGACCCGCTG 455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 979 AACGCTACATCAGCGCTGCTCAGTACGTACGTACGTACGTACGTACGTACGTAC 1038
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 456 CCGCAGAGAGAGCTGAGCGCATGATCCGAGGCGCGAGCGGAGAGAGAGAGAGAG 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1039 ACAATGAGAGAGTTGATGAATATGAAGAGACAGATGATGATGATGATGATGAT 1098
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 516 AACTACGAGAGAGTTGCGGAGAGATCTCGCCCGAGAGAGTGAAG 556
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1099 AACTATGAGAGTTTGTACAAATGATGACACCAAGAGGGGG 1139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 6
: Sequence 1, Application US/08818252B
: Patent No. 6197928
: GENERAL INFORMATION:
: APPLICANT: Tsien, Roger Y.
: APPLICANT: Miyawaki, Atsushi
: TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
: TITLE OF INVENTION: DETECTION OF ANALYTES
: FILE REFERENCE: 07257/042001
: CURRENT APPLICATION NUMBER: US/08/818.252B
: NUMBER OF SEQ ID NOS: 56
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1

```

```

: LENGTH: 1929
: TYPE: DNA
: ORGANISM: Aequorea victoria
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (0)...(1926)
: US-08-818-252-1

```

```

Query Match      14.3%; Score 122.6; DB 4; Length 1929;
Best Local Similarity 56.0%; Pred. No. 9e-16;
Matches 258; Conservative 0; Mismatches 194; Indels 9; Gaps 1;

```

```

QY 105 GAGCAGGATGCGCGGTGAGCTGCTCTGAGAGAGAGCCCACTACAAAGGCTTTC 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 679 GCCCGCCGATGATGACCAACTGACAGAGAGATTCGAGATTCAGAAAGCCCTTC 738
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 165 TCCCGGTTGACAGGATGGAAGGCGACATCAATGCCAGAGAGCTGGGCGCGCTG 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 739 TCATTATTCGACAGATGGGAGCGGACCATCCACCAAGAACTTGGACCGTTATG 798
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 225 AAGCCAGGCGCAAGAACTCTCGAGGCGCAGCTAAGAACTCATCTCCGAGTTGAC 284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 799 AGTCGCTTGACAAACCCCAAGCAAGCAATTCGAGATGATGATCAATGAAGTCAT 858
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 285 AGCGAGCGCGGCGGAATAGCTTCAGAGATTCCTGAGCGG-----GCAAG 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 859 GCTATGCAATGGAACGATTACTTCTGTAATTTCTTACTATGATGGCTAGAAAATG 918
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 336 AAGCCAGGCGCGCGCTGAGAGACCTGCGAGCTGCTCCGCGCTTCGACAGATGAC 395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 919 AAGGACACAGACAGCAAGAGAAATCCGAGAACATTCCTGTTTGGACAAAGATGG 978
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 396 GACGCGCATCATCCGTGAGAGAGCTCAGCGGCGCATGGCGGCGTGGGAGCCGCTG 455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 979 AACGCTACATCAGCGCTGCTGAAATGATGATGATGATGATGATGATGATGATGAT 1038
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 456 CCGCAGAGAGAGCTGAGCGCATGATCCGAGGCGCGAGCGGAGAGAGAGAGAGAG 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1039 ACAATGAGAGAGTTGATGAATATGAAGAGACAGATGATGATGATGATGATGAT 1098
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 516 AACTACGAGAGAGTTGCGGAGAGATCTCGCCCGAGAGAGTGAAG 556
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1099 AACTATGAGAGTTTGTACAAATGATGACACCAAGAGGGGG 1139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 7
: Sequence 5, Application US/08818252B
: Patent No. 6197928
: GENERAL INFORMATION:
: APPLICANT: Tsien, Roger Y.
: APPLICANT: Miyawaki, Atsushi
: TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
: TITLE OF INVENTION: DETECTION OF ANALYTES
: FILE REFERENCE: 07257/042001
: CURRENT APPLICATION NUMBER: US/08/818.252B
: NUMBER OF SEQ ID NOS: 56
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 1929
: TYPE: DNA
: ORGANISM: Aequorea victoria
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (0)...(1926)
: US-08-818-252-5

```

```

Query Match      14.3%; Score 122.6; DB 4; Length 1929;
Best Local Similarity 56.0%; Pred. No. 9e-16;
Matches 258; Conservative 0; Mismatches 194; Indels 9; Gaps 1;
QY 105 GAGCAGGATGCGCGGTGAGCTGCTCTGAGAGAGAGCCCACTACAAAGGCTTTC 164

```


QY 165 TCCTGGTTGACAGGATGAAAGCGACCATCAATGCCAGAGCTGGCGCGGCGCTG 224
DB 739 TCATTATTCGACAAAGATGGGAGCGCACATACACCAAGAACTTGGCACCGTTAG 798
QY 225 AAGGCCAGGCGCAAGAACCTCTCCGAGAGGCCAGCTAAGAAACTATCTCCGAGTTAC 284
DB 799 AGGTGCTTGGACAAACCAAGGAGCAAGATTCAGAGATATGATCAATGAAGTCAT 858
QY 285 AGCGAGCGGAGCGGCAATCAGCTTCCAGAGTCTTCCAGGCG-----GCAAG 335
DB 859 GCTGATGCAATGAGAACATTTACTTCTGATTTCTTACTATGATGGCTAGAAAAATG 918
QY 336 AAGCGAGGCGCGGCTTGGAGAGCTGAGTCCGCTTCCGCGCTTCCAGCAGAGATGCG 395
DB 919 AAGGACACAGACAGGAGGAAATCCGAGAAAGCATTCCTGTTTGGACAAAGATGG 978
QY 396 GACGCGCATATCAGCTGAGAGAGCTCAGGGGCGCATGGGCGCTGGGAGCGCGCTG 455
DB 979 AAGCGCTATCATCAGCGCTGCTGTAATTAAGTACGTCATGACAAACCTGGGAGAGTTA 1038
QY 456 CCGCAGAGAGAGCTGAGCGCATGATCCGAGCGAGCGGAGCTGAGCAGAGCGGCGGTG 515
DB 1039 ACAGATGAAGAAGTTGATGAATATGAAGGAGACGATATGATGATGGCCAACTA 1098
QY 516 AACTACGAGAGTTCGCGAGATGCTGCCCGCAGAGATAGG 556
DB 1099 AACTATGAAGATTGTACAATGATGACAGCAAGGGGG 1139

RESULT 10

US-08-818-253-7
Sequence 7, Application US/08818253
Patent No. 5998204
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,253
FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/043001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1971 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: Coding Sequence
LOCATION: 1...1968
US-08-818-253-7

Query Match 14.3%; Score 122.6; DB 2; Length 1971;
Best Local Similarity 56.0%; Pred. No. 9.1e-16;
Matches 258; Conservative 0; Mismatches 194; Indels 9; Gaps 1;

QY 105 GACGAGCATGCGCGGAGCTGACTCTGAGAGGAGGAGCCAGTACAAAAGGCTTTC 164
DB 727 GCGCGCCCATGCAATGACCACTGACAGAAAGAGATTCGAGATTCAAAAGACCTTC 786
QY 165 TCCTGGTTGACAGGATGAAAGCGACCATCAATGCCAGAGAGCTGGCGCGGCGCTG 224
DB 799 AGGTGCTTGGACAAACCAAGGAGCAAGATTCAGAGATATGATCAATGAAGTCAT 858
QY 225 AAGCGAGGCGGCAAGAACCTCTCCGAGAGCTTCCAGGCG-----GCAAG 335
DB 847 AGGTGCTTGGACAAACCAAGGAGCAAGATTCAGAGATATGATCAATGAAGTCAT 906
QY 285 AGCGAGCGGAGCGGCAATCAGCTTCCAGAGTCTTCCAGGCG-----GCAAG 335
DB 907 GCTGATGCAATGAGAACATTTACTTCTGATTTCTTACTATGATGGCTAGAAAAATG 966
QY 336 AAGCGAGGCGCGGCTTGGAGAGCTGAGTCCGCTTCCGCGCTTCCAGCAGAGATGCG 395
DB 967 AAGGACACAGACAGGAGGAAATCCGAGAAAGCATTCCTGTTTGGACAAAGATGG 1026
QY 396 GACGCGCATATCAGCTGAGAGAGCTCAGGGGCGCATGGGCGCTGGGAGCGCGCTG 455
DB 1027 AAGCGCTATCATCAGCGCTGCTGTAATTAAGTACGTCATGACAAACCTGGGAGAGTTA 1086
QY 456 CCGCAGAGAGAGCTGAGCGCATGATCCGAGCGAGCGGAGCTGAGCAGAGCGGCGGTG 515
DB 1087 ACAGATGAAGAAGTTGATGAATATGAAGGAGACGATATGATGATGGCCAACTA 1146
QY 516 AACTACGAGAGTTCGCGAGATGCTGCCCGCAGAGATAGG 556
DB 1147 AACTATGAAGATTGTACAATGATGACAGCAAGGGGG 1187

RESULT 11

US-08-818-252-7
Sequence 7, Application US/08818252B
Patent No. 6197928
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/08/818,252B
CURRENT FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1971
TYPE: DNA
ORGANISM: Aequorea victoria
FEATURE:
NAME/KEY: CDS
LOCATION: (0)...(1968)
US-08-818-252-7

Query Match 14.3%; Score 122.6; DB 4; Length 1971;
Best Local Similarity 56.0%; Pred. No. 9.1e-16;
Matches 258; Conservative 0; Mismatches 194; Indels 9; Gaps 1;

QY 105 GACGAGCATGCGCGGAGCTGACTCTGAGAGGAGGAGCCAGTACAAAAGGCTTTC 164
DB 727 GCGCGCCCATGCAATGACCACTGACAGAAAGAGATTCGAGATTCAAAAGACCTTC 786
QY 165 TCCTGGTTGACAGGATGAAAGCGACCATCAATGCCAGAGAGCTGGCGCGGCGCTG 224

```

Db 787 TCATTATGACAGAGATGGGGACGCGACATCACCACAAAGAACTTGGACCCGTTATG 846
QY 225 AAGGCCACGGCCAGAACCTCTCGAGGCCACCTAAGAACTATCTCCAGGTTGAC 284
Db 847 AGTGTGCTTGGACAAAACCAACGGAAGCAATTCAGAAATGATGATCAATGATGAT 906
QY 285 AGCGACGGCGGACGGAATTCAGCTTCAGAGTTCTCGAGCGCG-----GCAAGG 335
Db 907 GCTGATGGCAATGGAACGATTACTTCTCTGATTTCTTACTATGATGCTGAGAAAAATG 966
QY 336 AAGGCCAGGGCGGCGCTGAGACCTGACAGTCGCTCGCGGCTTCGACACAGATGCG 395
Db 967 AAGGACACAGACGAGCAAGAAATCGAAGAACATTCGTTGTTTGAACAAGATGGG 1026
QY 396 GACGGCCATACCTGACGACGCTCAGCGGGCCATGCGGGGCTGGGGGACCGCTG 455
Db 1027 AACGGCTACATAGCGCTCTCAGTACGTCACGTCATGACAAACCTCGGGGAGAGTTA 1086
QY 456 CCGCAGAGAGCTGAGCCCATGATCCGAGGCGGACGCTGAGCAGGCGGGGTTG 515
Db 1087 ACAGATGAAGAACTGATTAATGATAGGAAAGCAATGATGATGATGATGATGATG 1146
QY 516 AACTACGAGAGTTCGCGAGATGCTCGCCAGGAGTGAAG 556
Db 1147 AACTATGAAGAGTTTGTACAAATGATGACAGCAAGAGGGGG 1187

```

RESULT 12
US-08-100-874-1
Sequence 1, Application US/08100874
Patent No. 5498533

GENERAL INFORMATION:
APPLICANT: Poovalah, B. W.
APPLICANT: Takezawa, D.
APPLICANT: Han, T. J.
APPLICANT: An, G. H.
TITLE OF INVENTION: Control of Growth and Development of
TITLE OF INVENTION: Potato Plants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce
STREET: P. O. Box 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: USA
ZIP: 48303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,874
FILING DATE: July 30, 1993
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Smith, Dean F.
REFERENCE/DOCKET NUMBER: 7555-00004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 641-1600
TELEFAX: (313) 641-0270
TELEX: 287637 Harness UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 906 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ORIGINAL SOURCE: Solanum tuberosum

INDIVIDUAL ISOLATE: P-PCM-1
FEATURE:
NAME/KEY: CDS
LOCATION: 81..530
US-08-100-874-1

Query Match 12.9%; Score 110.4; DB 1; Length 906;
Best Local Similarity 54.6%; Pred. No. 26-13;
Matches 247; Conservative 0; Mismatches 196; Indels 9; Gaps 1;

```

QY 114 ATGCGCGGTAGCTGACTCTCTGAGAGGAGGCCACCTACAAAAAGCTTCTCCGGGTT 173
Db 81 ATGGCAGACAGCTGACGAGGAGCGAGATCGCGAGTTCAGAAAGACTTTTACCTTTTC 140
QY 174 GACACGATGGAAGGACGACATCATGCTCCAGAGACTGGCGGCGCTGAAAGCCAG 233
Db 141 GACAAAGATGGCGATGCTGATTAATACCAAGAGATTGGGAACAGTATGATGATCTT 200
QY 234 GGCAGAACTCTCGAGGCGCCAGCTAAGAAACTATCTCCAGGTTGACAGCAGGC 293
Db 201 GGTCAATATCCCTAGCTGACGATGACAGATGATGATGATGATGATGATGATGATG 260
QY 294 GACGCGAAATCAGCTTCCAGAGTTCTGA-----CGCGGCAAGAAAGCCAGG 344
Db 261 AATGGAACCATGATGATTTTCCAGAGTTCTGAATCTGATGACGTAAGATGAAGGAC 320
QY 345 GCGGCGCTGAGAGCTGAGGCTCGGCTCCGCGCTTGACACGAGATGGCGGCGCAC 404
Db 321 GATTCGAGAGGAGACTCAAAAGGCTTTCAGAGTTTGCATTAAGATCAGATGCTTT 380
QY 405 ATCACCCTGAGAGCTCAGCGCGCCATGAGCGGCGTGGCGAGCCGCTGCGCAGAG 464
Db 381 ATTTCTGACAGCTGAGCTTGCTGATTAATGACAAAGCTTGGAGAGAGCTGATGAA 440
QY 465 GAGCTGAGCGCATGATTCGCGAGCGCGAGCTGACAGAGAGCGGGGCTGAACGAG 524
Db 441 GAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 500
QY 525 GAGTTCGAGAGATGCTCGCGCCAGGAGTGAAG 556
Db 501 GAGTTTGTCCGATGATGCTTCCCAAGTGAAG 532

```

RESULT 13
US-09-239-909-1
Sequence 1, Application US/09239909
Patent No. 6284952

GENERAL INFORMATION:
APPLICANT: Kumho Petrochemical Co. Ltd.
TITLE OF INVENTION: Transgenic Plants with Divergent SCAM4 or SCAM5 Gene to Achieve
FILE REFERENCE: P99-2-6
CURRENT APPLICATION NUMBER: US/09/239,909
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: EP 99300136.1
NUMBER OF SEQ ID NOS: 4
SOFTWARE: KOPATIN 1.0
SEQ ID NO: 1

LENGTH: 1401
TYPE: DNA
ORGANISM: G. max calmodulin4 (SCAM4)
FEATURE:
NAME/KEY: CDS
LOCATION: (657)..(1106)
US-09-239-909-1

Query Match 11.0%; Score 94.8; DB 4; Length 1401;
Best Local Similarity 53.0%; Pred. No. 2-10;
Matches 232; Conservative 0; Mismatches 197; Indels 9; Gaps 1;

```

QY 113 CATGGCGGTGAGCTACTCTGAGAGAGGCGCCAGTACAAAAAGCTTCTCCCGGT 172
Db 656 CATGGCAGATATCTGATGAGAGAACAGATTTGATTTTAAAGAGCCCTTGGCTTGT 715

```

QY 173 TGACAGGATGAAACGGCCACCATATGCCAGAGCTGGCGCGCTGAAGCCAC 232
 Db 716 TGACAAATGAGATGCTGATCTAGTGAAGAACTTGCATCTGATCGTCAAT 775
 QY 233 GGGCAAGAACCTCTCGAGGCGCCAGCTAAGAAACTATCTCCAGAGTTGACAGGAGG 292
 Db 776 GGATTCAGAACCCCACTGAGAAAGAGCTCAAGATATGATTAAGAGTCGATGCGATGG 835
 QY 293 CGAGCGGCAATACGCTTCAGAGATTCCTGA-----CGCGCGGCAAGAAAGCCAG 343
 Db 836 CAATGGAAACCAATTTGATTTGACGATTTCTTGAGCTTGATGGCCAAAGAAAGTTAAAGAC 895
 QY 344 GGGCGGCTGAGAGACCTGCAAGGTCGCTCCGCGCTTCGACCAAGATGGCGAGGCCA 403
 Db 896 TGATGCAAGAGGAGGAGCTCAAGAAAGCTTCAAGGTTTTCGCAAAAGATCAAAATGGCTA 955
 QY 404 CATCACCTGAGACGAGCTCAGGCGCGCCATGGCGGGCTGGGGCAGCGCTGCGCAGGA 463
 Db 956 CATATCAGCTAGTGTGATGAGACAGATGATGATCAATATAGGGGAAACTAACCAGATGA 1015
 QY 464 GAGCTGAGCCCATGATCCCGAGGCGGAGCTGAGCCAGGAGCGGCGTGAAGTACGA 523
 Db 1016 AGAGTGGAGCAGATGATTAAGAAAGCAGATTTGGACGCTGATGGCCAAAGTTACTATGA 1075
 QY 524 GGAAGTGGCGAGATGCT 541
 Db 1076 GGAATTCGTCAAGATGAT 1093

RESULT 14

US-09-239-909-3
 : Sequence 3, Application US/092399909
 : Patent No. 6284952
 : GENERAL INFORMATION:
 : APPLICANT: Kumo Petrochemical Co. Ltd.
 : TITLE OF INVENTION: Transgenic Plants with Divergent SCAM4 or SCAM5 Gene to Achieve N

: FILE REFERENCE: p99-2-6
 : CURRENT APPLICATION NUMBER: US/09/239, 909
 : CURRENT FILING DATE: 1999-01-29
 : EARLIER APPLICATION NUMBER: EP 99300136.1
 : EARLIER FILING DATE: 1999-01-08
 : NUMBER OF SEQ ID NOS: 4
 : SOFTWARE: KOPATIN 1.0
 : SEQ ID NO 3
 : LENGTH: 916
 : TYPE: DNA
 : ORGANISM: G. max calmodulin5 (SCAM5)
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (69)..(518)
 : US-09-239-909-3

Query Match 10.3%; Score 88.4; DB 4; Length 916;
 Best Local Similarity 52.1%; Pred. No. 3.7e-09;
 Matches 226; Conservative 0; Mismatches 201; Indels 9; Gaps 1;

QY 113 CATGCGCGTGTGAGTCTGCTGAGAGAGAGCCAGTACAAAGAGCTTCTCCGCGGT 172
 Db 68 CATGGCAGATGCTGTGAGTGAAGAAAGATAGTGAATCAAGAAAGCTTTGGCTTGT 127
 QY 173 TGACAGGATGAAACGGCCACCATATGCCAGAGAGTGGCGCGCTGAAGGCCAC 232
 Db 128 TGACAAAGATGATGATGGCTCATTTAGCTGAGCAATTTGTCACGGTTATCCGGTCAAT 187
 QY 233 GGGCAAGAACCTCTCGAGGCGCCAGCTAAGAAACTATCTCCAGGTTGACAGGAGCG 292
 Db 188 GGTTCAGAACCCCAAGAAAGAGCTTCAAGACATGATTAAGAGAGTGAAGTGAAGATGG 247
 QY 293 CGAGCGGCAATACGCTTCAGAGTTCCTGA-----CGCGCGGCAAGAAAGCCAG 343
 Db 248 TAAATGAAACCAATGATTTGTTGAGTTTGAAGCTTAATGGCAAAAGATGAAGGAAC 307

QY 344 GGGCGGCTGAGAGACCTGCAAGTCCCTCCGCGCTTCGACCAAGATGGCGAGGCCA 403
 Db 308 TGATGAAAGAGAAATCTCAAGAGAGGCTTTCAGGTGTTGACAAAGATCAAAATGGCTA 367
 QY 404 CATCACCTGAGACGAGCTCAGGCGCGCCATGGCGGGCTGGGGCAGCGCTGCGCGAGGA 463
 Db 368 CATTTCAAGCAAGTGTGATGAGACACGTTATGATCAATGTGGGTGAAAACCTACTGATGA 427
 QY 464 GAGCTGAGCCCATGATCCCGAGGCGGAGCTGAGCCAGGAGCGGCGGTGAAGTACGA 523
 Db 428 GAGGTGGAGCAGATGATTAAGAAAGCAGATTTGGATGATGATGATCAAGTTAATATGA 487
 QY 524 GGAAGTGGCGAGATGCT 541
 Db 488 TGAATTTGTCAAGATGAT 505

RESULT 15

US-08-993-380-3
 : Sequence 3, Application US/08993380B
 : Patent No. 6077676
 : GENERAL INFORMATION:
 : APPLICANT: Shi, Qian-Li
 : TITLE OF INVENTION: SINGLE CHAIN POLYPEPTIDES COMPRISING TROPONIN I AND

: FILE REFERENCE: 1112-1-053
 : CURRENT APPLICATION NUMBER: US/08/993, 380B
 : CURRENT FILING DATE: 1997-12-18
 : NUMBER OF SEQ ID NOS: 6
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 3
 : LENGTH: 1173
 : TYPE: DNA
 : ORGANISM: Homo sapiens (modified)
 : US-08-993-380-3

Query Match 9.1%; Score 78.2; DB 3; Length 1173;
 Best Local Similarity 53.3%; Pred. No. 3.6e-07;
 Matches 201; Conservative 0; Mismatches 158; Indels 18; Gaps 1;

QY 180 GATGAAGAGCCACCATCAATGCCAGAGAGCTGGCGCGCGGCTGAAGAGCCAGCGGCAAG 239
 Db 778 GCTGAGATGCTGATGATGAGCAGCAGAGAGCTGGCGCAAGAGTATGATGATGCTGGCCAG 837
 QY 240 AACCTCTGAGAGCCCACTAAGAAACTCATCTCCAGGTTGACAGGAGCGGAGCGC 299
 Db 838 AACCCACCCCTGAGAGAGCTGCAAGAGATGATGATGATGATGATGATGATGATGATGATG 897
 QY 300 GAATCAGCTTCCAGAGAGTCTGACGCGCGCAAGAGAGCCAGCGCGCT----- 352
 Db 898 ACGGTGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 957
 QY 353 -----GAGAGACCTGAGAGCTGCGCTTCCGCGCTTCGACCAAGATGGAGCGGC 401
 Db 958 GGGAAATGTGAGAGAGAGCTTCTGACCTTCTCCGATGTTTGAACAAATGCTGATGGC 1017
 QY 402 CACATCAGCTGAGAGAGCTGAGCGGCGCATGAGCGGCGCTGAGGAGCGCGCTCCGCGAG 461
 Db 1018 TACATGACCTGATGATGAGCTGAAGTAAATGCTGAGGCTTACAGGACCATCATCAGGAG 1077
 QY 462 GAGAGAGCTGAGAGCGCATGATCCGAGGCGCGCATGAGCGGCGCATGAGCGGCGGTAACTAC 521
 Db 1078 GACACACATCGAGAGCTTCATCAAGAGAGGAGAGCAAGAAACAGAGCGCGCATGATGAT 1137
 QY 522 GAGAGTTCGAGAGAT 538
 Db 1138 GATGAGTTCGAGATTT 1154

Search completed: May 16, 2003, 01:36:21
 Job time : 91 secs

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

9214.099 Million cell updates/sec

Sequence: 1 aattccgataccctgcgc.....aggaactgcgagttcca aa 858

Scoring table: IDENTITY_NUC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

	Gentiana1.*
1.	gb.ba1.*
2.	gb.htg.*
3.	gb.in.*
4.	gb.om.*
5.	gb.ov.*
6.	gb.pat.*
7.	gb.ph.*
8.	gb.pl.*
9.	gb.pr.*
10.	gb.ro.*
11.	gb.sts.*
12.	gb.sy.*
13.	gb.un.*
14.	gb.v1.*
15.	em.ba.*
16.	em.fun.*
17.	em.hum.*
18.	em.in.*
19.	em.mu.*
20.	em.om.*
21.	em.or.*
22.	em.ov.*
23.	em.pat.*
24.	em.pl.*
25.	em.pl1.*
26.	em.ro.*
27.	em.sts.*
28.	em.un.*
29.	em.v1.*
30.	em.htg_hum.*
31.	em.htg_inv.*
32.	em.htg_other.*
33.	em.htg_mus.*
34.	em.htg_pln.*
35.	em.htg_rod.*
36.	em.htg_mam.*
37.	em.htg_virt.*
38.	em.sy.*
39.	em.htgo_hum.*
40.	em.htgo_mus.*
41.	em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match	Length	DB	ID	Description
1	858	100.0	858	6	AX077138	AX077138 Sequence
2	858	100.0	858	9	AF172852	AF172852 Homo sapi
3	843.4	98.5	913	6	AX399961	AX399961 Sequence
4	843.4	98.3	185926	2	AL732437	AL732437 Homo sapi
5	211.2	24.6	1306	6	AX333250	AX333250 Sequence
6	211.2	24.6	1306	6	AX334352	AX334352 Sequence
7	211.2	24.6	1306	6	AX335626	AX335626 Sequence
8	211.2	24.6	1306	9	HUMN1	M8026.Human NB-1
9	211.2	24.6	1316	9	BC031889	BC031889 Homo sapi
10	211.2	24.6	2739	9	HUMCALP5	M6707.Human calmo
c 11	211.2	24.6	185926	2	AL732437	AL732437 Homo sapi
12	209.6	24.4	2746	6	AX335631	AX335631 Sequence
13	209.6	24.4	2746	6	HSCAMP5G	X13461.H.sapiens
c 14	185.4	21.6	106359	2	AC103443	AC103443 Rattus no
15	181.2	21.1	1519	3	MPCAN	X85091.M.pyritifera
16	178.2	20.8	1111	3	TCOCALB2	X52096.Trypansoma
17	174.6	20.3	899	10	AB036744	AB036744 Mus muscu
18	172.8	20.1	743	8	ZMRNBL7	X74490.Z.mays mRNA
19	172.6	20.1	1358	8	PHITCALP1A	M63535.P.intestans
20	170.2	19.8	1439	8	BC005457	BC005457 Mus muscu
21	169.2	19.7	1357	3	AY118890	AY118890 Drosophila
22	169	19.7	824	8	AF042840	AF042840 Oryza sat
23	169	19.7	2175	9	HUMCAMA	X04046.Human calmo
24	169	19.7	2190	7	BC005137	BC005137 Homo sapi
25	167	19.5	691	10	RSPRCMA	X13817.H.norvegicu
26	166.2	19.4	599	10	RATCAMB	M16659.Rat calmodu
27	166	19.3	450	5	ELCCALMA	M36168.E.electricu
28	166	19.3	883	5	ELCCAMEEL	X00931.E.electricu
29	165.4	19.3	542	8	AF007889	AF007889 Sybiodiod
30	165.2	19.3	616	3	LTCNAA	X80231.L.tarentolia
31	165.2	19.3	722	10	MUSCALINDA	M19380.Mouse calmo
32	164.6	19.3	447	3	DMCANR	Y00133.Drosophila
33	162.6	19.0	841	8	TAU45105	U49105.Tritilicum ae
34	162.2	18.9	775	8	OSU79326	X7936.Oryza sativ
35	162.2	18.9	961	8	AF231026	AF231026 Oryza sat
36	161.6	18.8	480	8	AF031482	AF031482 Zea mays
37	159.6	18.6	1644	5	AF085250	AF085250 Perca fla
38	159.6	18.6	106359	2	AC103443	AC103443 Rattus no
39	158	18.4	450	5	CHKM11	K00510.Chicken CCM
40	158	18.4	595	12	SYNARBCAL	J04729.A.punctulata
41	158	18.4	1038	3	BF133836	AJ133836 Branchios
42	157	18.3	1322	3	LRU291615	AJ291615 Lumbricus
43	156.4	18.2	1037	7	BIA133486	X133486 Branchios
44	156.2	18.2	775	8	ZMCAN2	X73397.Z.mays CAM2
45	155.6	18.1	409	5	ORZCAMA	D10363.O.lalipes

ALIGNMENTS

RESULT	1
AX077138	
LOCUS	AX077138
DEFINITION	Sequence 2. from Patent WO0107604.
ACCESSION	AX077138
VERSION	AX077138.1 GI:13121753
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 858) Mehuli B., Bernard D. and Simonetti L. Isolated peptide of the horny layer and use thereof Patent: WO 0107604-A 2 01-FEB-2001;
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	

QY 361 TGCAGTGCCTTTCGCGCCCTTGCAGCAGAGATGGCGAGCGGCACATCACCTGGAGAC 420
 DB 361 TGCAGTGCCTTTCGCGCCCTTGCAGCAGAGATGGCGAGCGGCACATCACCTGGAGAC 420
 QY 421 TCAGGCGGCGCATTCGCGGCGCTGGGGCAGCCCTGCGCGAGAGAGCTGGAGCGCATTA 480
 DB 421 TCAGGCGGCGCATTCGCGGCGCTGGGGCAGCCCTGCGCGAGAGAGCTGGAGCGCATTA 480
 QY 481 TCAGGAGAGCGCAGCTGAGCAGAGAGCGGCGGTGAACACAGAGAGATTGCGAGAGATGC 540
 DB 481 TCAGGAGAGCGCAGCTGAGCAGAGAGCGGCGGTGAACACAGAGAGATTGCGAGAGATGC 540
 QY 541 TCAGCAGAGAGATGAGAGCTCCCGCCTGTGTCTCCCTGCGCTGTGAGCCTTCAGGCG 600
 DB 541 TCAGCAGAGAGATGAGAGCTCCCGCCTGTGTCTCCCTGCGCTGTGAGCCTTCAGGCG 600
 QY 601 CACCGCGCGCTGCTGCTTTTGTGCTGGAGCTCTCGGGGAAACCTGTGTGTGATGGA 660
 DB 601 CACCGCGCGCTGCTGCTTTTGTGCTGGAGCTCTCGGGGAAACCTGTGTGTGATGGA 660
 QY 661 AACTGCTCCCGCTGCGGAGAGAGGCTTTCGCTCCGCGGCGCTGAGATGGCGCGCTCGGG 720
 DB 661 AACTGCTCCCGCTGCGGAGAGAGGCTTTCGCTCCGCGGCGCTGAGATGGCGCGCTCGGG 720
 QY 721 CGCGCTGCGAGCGCCCTCTCTGCTTCAGACTTGGGCGAGAGAGCGCTCTTGGGCGCTG 780
 DB 721 CGCGCTGCGAGCGCCCTCTCTGCTTCAGACTTGGGCGAGAGAGCGCTCTTGGGCGCTG 780
 QY 781 GTCCCGCTTTCGCTGCTGCACTGGAATGAGGCGCCCTTAACCCCGCATTTAATAAAG 840
 DB 781 GTCCCGCTTTCGCTGCTGCACTGGAATGAGGCGCCCTTAACCCCGCATTTAATAAAG 840
 QY 841 GACTGCGGAGTTCAGAAA 858
 DB 841 GACTGCGGAGTTCAGAAA 858

RESULT 3
 LOCUS AX399961 913 bp DNA linear PAT 06-JUN-2002
 DEFINITION Sequence 132 from Patent WO0218424.
 ACCESSION AX399961
 VERSION AX399961.1 GI:21336273
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 AUTHORS Tang,Y.T., Asundi,V., Zhou,P., Xue,A.J., Ren,F., Zhang,J., Wang,J.R., Zhao,Q.A., Wang,D., Liu,C., Drmanac,R.T. and Wehman,T.
 TITLE Nucleic acids and polypeptides
 JOURNAL Patent: WO 0218424-A 132 07-MAR-2002;
 HYSEQ, INC. (US)

FEATURES
 source Location/Qualifiers
 1..913

CDS
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 162..602
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD33405.1"
 /db_xref="GI:21336274"
 /translation="MAGELTPEEEAOYKKASAVTDGNTINOELGAALKATGKNL
 SEADLRKISFVSDSGEISFOEFLTAKKARAGLELDLQAFRAFDDGDGCHITVDE
 LRRMAGIGQPLPDELDAMTREADVDGGRVNEEFARMLAOE"

BASE COUNT 175 a 279 c 321 g 138 t
 ORIGIN

Query Match 98.5%; Score 844.8; DB 6; Length 913;
 Best Local Similarity 99.2%; Pred. No. 1.4e-106;
 Matches 849; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TTCCCGGATCCCTGCGGCTGCTGCACCTGTGACACAGAGCTCTGAGACAGAGGTGA 62
 DB 51 TGCCCGGATCCCTGCGGCTGCTGCACCTGTGACACAGAGCTCTGAGACAGAGGTGA 110
 QY 63 GGGCGGCTGGGACAGACTCGAGAGCTCCGCGAGGTGACAGAGACAGGATGGCGGT 122
 DB 111 GGGCGGCTGGGACAGACTCGAGAGCTCCGCGAGGTGACAGAGACAGGATGGCGGT 170
 QY 123 GAGCTACTCTGAGAGAGAGGCGCCAGTACAAAAGGCTTTTCCCGGGTTGACAGCGAT 182
 DB 171 GAGCTACTCTGAGAGAGAGGCGCCAGTACAAAAGGCTTTTCCCGGGTTGACAGCGAT 230
 QY 183 GGAAGGACCATCATCAATGCCAGAGACTGGGCGCGCTGAGAGCCAGCGCAAGAAC 242
 DB 231 GGAAGGACCATCATCAATGCCAGAGACTGGGCGCGCTGAGAGCCAGCGCAAGAAC 290
 QY 243 CTCTCGAGGCGCCAGCTAAGAAATCTATCTCCGAGTTGACAGCGACGGCGCA 302
 DB 291 CTCTCGAGGCGCCAGCTAAGAAATCTATCTCCGAGTTGACAGCGACGGCGCA 350
 QY 303 ATCAGCTTCAGAGAGTTCCTGACGCGCGGCAAGGAGGCGGCGCTGAGAGACTG 362
 DB 351 ATCAGCTTCAGAGAGTTCCTGACGCGCGGCAAGGAGGCGGCGCTGAGAGACTG 410
 QY 363 CAGGTGCGCTTCGCGCCTTCGACAGATGGCGAGCGCACATCACCGTGGACGACTC 422
 DB 411 CAGGTGCGCTTCGCGCCTTCGACAGATGGCGAGCGCACATCACCGTGGACGACTC 470
 QY 423 AGCGGGCCATGGCGGGGCTGGGGCAGCGCTGCGCGAGAGAGAGCTGACGCCATGATC 482
 DB 471 AGCGGGCCATGGCGGGGCTGGGGCAGCGCTGCGCGAGAGAGAGCTGACGCCATGATC 530
 QY 483 CGGAGGCGCGAGCTGAGACAGAGAGCGGGGGTGAATACAGAGAGTTGCGAGAGATGCTC 542
 DB 531 CGGAGGCGCGAGCTGAGACAGAGAGCGGGGGTGAATACAGAGAGTTGCGAGAGATGCTC 590
 QY 543 GCCCAGAGTGAAGGCTCCCGCCTGTGTCCCTCGCTGCTGAGCTTCAGGCGCA 602
 DB 591 GCCCAGAGTGAAGGCTCCCGCCTGTGTCCCTCGCTGCTGAGCTTCAGGCGCA 650
 QY 603 CGCGCGCTGCTGCTTTTGTGCTGGAGACTCTCCGGGAAACCTGTGCGGTGATGGGAAA 662
 DB 651 CGCGCGCTGCTGCTTTTGTGCTGGAGACTCTCCGGGAAACCTGTGCGGTGATGGGAAA 710
 QY 663 CTGCGTCCCGCTGGGAGAGAGGCTTGGCTCCGGGGCGTGGATGGGGCGCTCGGGCC 722
 DB 711 CTGCGTCCCGCTGGGAGAGAGGCTTGGCTCCGGGGCGTGGATGGGGCGCTCGGGCC 770
 QY 723 GCTGCGAGCGCCCTCTCTGCTTCAGACCTTGGGCGAGAGAGGCGCTTGGGCGTGT 782
 DB 771 GCTGCGAGCGCCCTCTCTGCTTCAGACCTTGGGCGAGAGAGGCGCTTGGGCGTGT 830
 QY 783 CCGCTTTTGGCTGCACTGATGAGAGGCGCCCTTAACCCCGCATTTATTAATAAGCA 842
 DB 831 CCGCTTTTGGCTGCACTGATGAGAGGCGCCCTTAACCCCGCATTTATTAATAAGCA 890
 QY 843 CTGCGGAGTTCAGAAA 858
 DB 891 CTGCGGAGTTCAGAAA 906

RESULT 4
 LOCUS AL732437 185926 bp DNA linear HTG 16-AUG-2002
 DEFINITION Homo sapiens chromosome 10 clone RP11-11668, *** SEQUENCING IN
 PROGRESS ***, 2 unordered pieces.
 ACCESSION AL732437
 VERSION AL732437.11 GI:22316190
 KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

Db	119	CCCTGGCATTGGCCCGCACCGCTGACTGAGGACAGGTACACAGATTCAAGAGAGCCTTCTC	178
QY	167	CGCGGTTGCACACGGATGTAAGAAACGGCACCATCAATATGCCAGGAGCTGGGCGCGCGTTGAA	226
Db	179	CCTGTTTGCACAAGGATGGGGACGGCTGCATCACACCGCGAGGCTGGGACAGGTCATCG	238
QY	227	GGCCACGGGGCAAGAACCTCTCTGGGAGGGCCAGCTAAGGAAACTCATCTCCGAGGTTGACAG	286
Db	239	GTCCTGGGCCAAGAACCCCGACGGAGGCCAGACTGGGGACATGATGAGTGCATGATGCACCG	298
QY	287	CGACGGCGACCGGCAATACAGTTCACAGGAGTTC-----TGAGGGGGGCAAGGAA	337
Db	299	GGACGGCGAACCGGCACCGGTGACTTCCCGGAGTCTCTGGGCAATGATGCCAGAGAGATGAA	358
QY	338	GGCCAGGGCGCGCCTGAGAGACCTGCAGATGCCTTCCGCGCCTCTCGACACAGATGGCGA	397
Db	359	GGACACGGACAACGAGGAGAGATCCGGGAGGCTTCCGGCGTTCGACACAGGAGCGCAA	418
QY	398	CGGCGCACTCAACCGTGGACAGAGCTCAGGCGGGCCATGGCGGGGGCTGGGGGACCGCCTGCC	457
Db	419	CGGCTTCTCTCAACCGCGCGCGGACTAAGCACTAGCATGACCCGGCGGGGGAGAAACTAG	478
QY	458	GCAGGAGAGAGCTGACAGCGCATGATCCGGGAGGGCCACTGACACGACGAGCGGGGGTAA	517
Db	479	TGACGAGAGAGGTGACAGAGATGATCCGGGCGCGGACACAGGACGAGACGACAGGTAA	538
QY	518	CTACGAGGAGTTCCGGAGGATCTCGCCCAAGAGTGAAGGCTCCCGCGCTGATGCCCTCG	577
Db	539	CTACGAGGAGTTTGCCTGTGCTGTGTCCAAAGTAGAGGCGGCGGCCACCATGCTCTCG	598
QY	578	GCTGCGCTCTGAGCCTTCAGGGCCACCGCCGGCTGC	613
Db	599	GAGCGCCACGCGCGCCACAGGCGCAAGAACCGGGGCG	634

RESULT	6			
LOCUS	AX334352			
DEFINITION	AX334352 Sequence 4861 from Patent WO0194629.	1306 bp	DNA	linear
ACCESSION	AX334352			PAT 09-JAN-2002
VERSION	AX334352.1	GI:18125071		
KEYWORDS	human.			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G., Horrigan,S., Soppel,D.R. and Weaver,Z. Cancer gene determination and therapeutic screening using signature gene sets Patent: WO 0194629-A 4861 13-DEC-2001;			
TITLE	Avalon Pharmaceuticals (US) Location/Qualifiers			
JOURNAL	1. .1306			
FEATURES	/organism="Homo sapiens" /db_xref="taxon:9606"			
ORIGIN	BASE COUNT 258 a 434 c 403 g 211 t			
Query Match	24.6%; Score 211.2; DB 6;			
Best Local Similarity	64.7%; Pred. No. 5.4e-20;			
Matches 334; Conservative	0; Mismatches 173; Indels 9; Gaps 1;			

QY	227	GGCCACGGGGCAAGAAACCTCTGGAGAGGCCAGCTAAGAAACATCATCTCGAGAGTTGACAG	286
Db	239	GTCCCTGGGGCCAGAAACCCACGAGAGGCCGAGTGTGGGACATGATGATGATGATGATGACCG	298
QY	287	CGACGGCCACCGCGCAATCAGCTTCCAGAGTTCC-----TGACGGGGCCAGAGAA	337
Db	299	GGACGGCCAAACGGCAACCGCTGGACCTTCCCGGAGTTCTTGGGCAATGATGGCCAGGAAGATGAA	358
QY	338	GGCCAGGGGCGGACCTGGAAGACCTGCAAGTTCGCTTCCGCGGCTTTCGACCAGAGATGGCGA	397
Db	359	GGACACGGGACAAACGAGGAGAGATCCGAGAGGCTTCCGCGTGTTCGACAAAGAGACGGCAA	418
QY	398	CGGCCACACTCACCGCTGGACGACAGCTCAGGCGGGGCATGGCGGGGCTGGGGGACCGGCTGCC	457
Db	419	CGGCTTCCTTCACCGCGCGCCGAGCTACGACAGTCTACACCGGCTGGGGGGAGAACTGAG	478
QY	458	GCAGAGAGAGCGTGGACGCGCATGATCCGAGAGGCCACATCGACACGAGACGGGCGGTGAA	517
Db	479	TGACGAGAGAGGTGGACGAGATGATCCGGGCGCGGACACGGAACGGAGACGGAAGTGA	538
QY	518	CTACGAGGAGTTCGCGAGAGATGCTCGCCGAGAGATGAGAGCTCCCGCTGTGTCTCCCTG	577
Db	539	CTACGAGGAGTTTGTCCCTGTGCTGTGTTGCCAAGTGAAGGCGGCGCCACCATGATGCTCTG	598
QY	578	GCTGGGCTCTAGGCTTCAGGGGCCACGGCCGGCTGC	613
Db	599	GGCGCCCAACGGCGCCACAGGGCAAGAAACCGGGGC	634

RESULT 7					
AX335626					
LOCUS	AX335626	1306 bp	DNA	Linear	PAT 09-JAN-2002
DEFINITION	Sequence 6135 from Patent WO0194629.				
ACCESSION	AX335626				
VERSION	AX335626.1	GI:18126345			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1				
TITLE	Young,P.E., Augustus,M., Carter,K.C., Ebdner,R., Endress,G.,				
	Horrikan,S., Soppet,D.R. and Weaver,Z.				
	Cancer gene determination and therapeutic screening using signature				
JOURNAL	Patent: WO 0194629-A 6135 13-DEC-2001;				
FEATURES	Avalon Pharmaceuticals (US)				
source	Location/Qualifiers				
	1..1306				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
BASE COUNT	258 a 434 c 403 g 211 t				
ORIGIN					

Dbb 179 CCGTGTTCACACAGGATGGGACCGCTGCATCCACCCGCGAGCTGGGACACGGTCAATCG 238

QY	338	GGCCAGGGCCGGCCTTGAGAGACCTGCAAGATGCCCTTCGGCCCTTGACCAAGGATGGCGA	397
Db	359	GGACACGGACAAACAGGAGGAGATCCCGGAGCCTTCGCGCTGTTCACAAAGGACGGCAA	418
QY	398	CGGCCACATCACCGTTGGACGAGCTCAGGCGGGGCCATGGCGGGGCTGGGGCAGCCGCTGCC	457
Db	419	CGGGTTCTCTCCAGCCCGCGCGGCTACACACATGTCATACCCGGCTGGGGGGGAAGCTGAG	478
QY	458	GCAGAGAGAGCTGGACGCCATGATCCGCGAGGCGCGAGCTGGAGCAGGAGCGGCGGTGAA	517
Db	479	TGACAGAGGAGGTGGACGAGATGATCCGGGCGCGGACACGAGCGAAGACGACAGGTGAA	538
QY	518	CTACGAGGAGTTCGCGAGGATGCTCGCCCAAGAGTGAAGCTCCCGCCTGTGTCCCTCG	577
Db	539	CTACGAGGAGTTCGCTGCTGCTGGTGTCCAAAGTGAAGGCGCGCGCCACCACATGCTCTG	598
QY	578	GCTGCGGCTCTGAGCCTTCAGGAGCCACCGCCCGCTGCG	613
Db	599	GGCGGCCACGGCGCCACACAGGCGCAAGAACCCCGGGCG	634

RESULT	8
HUMNB1	
LOCUS	HUMNB1 1306 bp mRNA linear . PRI 27-APR-1993
DEFINITION	Human NB-1 mRNA, complete cds.
ACCESSION	M58026
VERSION	M58026.1 GI:189080
KEYWORDS	NB-1.
SOURCE	Human breast epithelia cell, cDNA to mRNA.
ORGANISM	Homo sapiens

REFERENCE	1 (pages 1 to 1306)
AUTHORS	Yaswen, P., Smoll, A., Peehl, D.M., Trask, D.K., Sager, R. and Stampfer, M. R.
TITLE	Down-regulation of a calmodulin-related gene during transformation of human mammary epithelial cells
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 87 (19), 7360-7364 (1990)
MEDLINE	91017505
PUBMED	2217169

FEATURES	Location/Qualifiers
source	1..1306 /organism="Homo sapiens" /db_xref="taxon:9606"
gene	1..1306 /gene="NB-1"
mRNA	<1..575 /gene="NB-1"
CDS	126..575

BASE COUNT	258 a	434 c	403 g	211 t
ORIGIN				

Query Match	24.6%;	Score 211.2;	DB 9;	Length 1306;
Best Local Similarity	64.7%;	Pred. No. 5.4e-20;		
Matches 334; Conservative	0;	Mismatches 173;	Indels 9;	Gaps 1

Dy 107 CGCAGGCATGGCCCGGTGACCTGACTCCTTAGGAGGAGGCCCACTACAAAAAGGCTTTC 166
| | | | | | | | | | | | | | | | | | | | |
Db 119 CCTGGCATGGCCGACCACACTGACTGAGGAGCAGCTCACAGAATTCAAGGAGGCCCTTC 178

Dy 167 CCGGGTTGACACCGGATGGAAACGCCACCATCAATCCCCAGAGCTGGGCGCGCGGTGA 226
| | | | | | | | | | | | | | | | | |
Db 179 CCTGTTTGACAAGGATGGGGACGGCTGCATCACCACCCGCGAGCTGGGCACGGTCATGCG 238

oy 227 GGGCAGGGCAAGAACCTCTCGGAGGCCAGCTAAGAACTCATCTCCGAGTTGACAG 286

Db	239	GTCCCTGGGCCAGAACCCCGAGGCCGAGCTGGGAGCATGATGAGTGCACCG	298
Qy	287	CGACGGCCACGGCCGCAATACAGCTTCAGAGAGTCC-----TGAGGGGGCCAGGAA	337
Db	299	GGACGGCAACGGCACCGTGACCTTCCCGAGTCTCTGGGCATGATGGCCAGGAGATGAA	358
Qy	338	GGCCAGGGCCGGCCCTGGAGGACCTTCAGAGTGCCTTTCGCGGCTTCGACAGAGATGGGA	397
Db	359	GGACACGGGCAACGAGGAGAGATCCGGAGGCGCTTCGCGGCTTCGACAAAGAGACGGCAA	418
Qy	398	CGGCCACATCAACCTGTGAGACGACTAGCGCGGCCATGGCGGGGCTGGGGGACGCCCTGCC	457
Db	419	CGGCTTCTGTACGCGCGCGGAGCTACGACACTCATYGACC CGGCTGGGGGGAACATCGAG	478
Qy	458	GCAGGAGGAGAGCTGAGAGCCATGATCCGCGAGGCGCCACGCTGACACGAGACGGGCGGGTAA	517
Db	479	TGACGAGGAGAGGTGGACGAGATGATCTCGGGCGCGCGGACACGAGGAGCGACAGTGA	538
Qy	518	CTACGAGGAGTTCGCGGAGATGCTTGCGCCAGGAGTGAAGGCTCCCGGCTGTGTCCCTCG	577
Db	539	CTACGAGGAGTGTTCGCTGTGTCTGTGTCCAAAGTGAAGGAGGCGCGGCCCAACCATGCTCTG	598
Qy	578	GCTGGCTGTGACCTTCAGGGGCCACCGCCGCGCTGC	613
Db	599	GGCGCCCAACGGGGCCACAGGGCAAGAACCCGGGGC	634

RESULT	9
LOCUS	BC031889
DEFINITION	BC031889 Homo sapiens, calmodulin-like 3, clone MGC:30093 IMAGE:477524,
ACCESSION	BC031889 mRNA linear PRI 27-JUN-2002
VERSION	BC031889 rRNA, complete cds.
KEYWORDS	BC031889.1 GI:21619432
SOURCE	MGC.
	human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1316)
Strausberg, R.
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK	COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov	
Contact: MGC help desk	
Email: cgapbs-remail.nih.gov	
Tissue Procurement: James Cleaver, M.D.	
cDNA Library Preparation: Life Technologies, Inc.	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNT)	
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center	
Center code: BCM-HGSC	
Web site: http://www.hgsc.bcm.tmc.edu/cdna/	

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRAK Plate: 42 Row: e Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 4885110.

```

FEATURES
SOURCE
Location/Qualifiers
1. 1316
/organism="Homo sapiens"
/db_xref="locusID:810"
/db_xref="taxon:9606"
/clone="MGC:30093 IMAGE:4777524"

```

CDs
 /tissue_type="Skin, normal"
 /clone_lib="NCI CGAP_Skn3"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6, ccdb"
 106, .555
 /codon_start=1
 /product="calmodulin-like 3"
 /protein_id="AAH3189.1"
 /db_xref="GI:21619433"
 /translation="MADLTIEQVTEFEKARSLEPKDGDCITTRLETQVRSIQNP
 TEALRDMSEIDRNGNTVDPEFLGMARKMDTDEEIRAEFRFDKNGEVS
 AAELRHVTRIGEKISDEVDENIRADTDSDGQVNEEFVRVIVSK"

BASE COUNT 280 a 427 c 399 g 210 t
 ORIGIN

Query Match 24.6%; Score 211.2; DB 9; Length 1316;
 Best Local Similarity 64.7%; Pred. No. 5.4e-20;
 Matches 334; Conservative 0; Mismatches 173; Indels 9; Gaps 1;

107 CGCAGCATGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCCAGTACAAAAGGCTTCTC 166
 99 CCTTGACATGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCCAGTACAAAAGGCTTCTC 158
 167 CGCGTTGACAGGATGGAACGCAACATCAATGCGCGGTGAGCGCGCGCTGAA 226
 159 CCTGTTGACAGGATGGAACGCAACATCAATGCGCGGTGAGCGCGCGCTGAA 218
 227 GCGCAGGCGCAAGAACCTCTCGAGAGCGCGCAATGAGAAACATCTCCGAGCTTACAG 286
 219 GTCCTGCGCGCAAGAACCTCTCGAGAGCGCGCAATGAGAAACATCTCCGAGCTTACAG 278
 287 CGACGCGCAGGCGCAAGAACCTCTCGAGAGCGCGCAATGAGAAACATCTCCGAGCTTACAG 337
 279 GACGCGCAGGCGCAGGCGCAAGAACCTCTCGAGAGCGCGCAATGAGAAACATCTCCGAGCTTACAG 338
 338 GCGCAGGCGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCCAGTACAAAAGGCTTCTC 397
 339 GACGCGCAGGCGCAGGCGCAAGAACCTCTCGAGAGAGAGCGCGCTTCCGCTGTTGACAGAGCGCA 398
 398 GCGCAGGCGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 457
 399 GCGCTTCTGACAGGCGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 458
 458 GCGAGAGGAGCTGAGAGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 517
 459 TGACGAGAGGAGCTGAGAGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 518
 518 CTACGAGAGGAGCTGAGAGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 577
 519 CTACGAGAGGAGCTGAGAGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 578
 578 GCTGCGCTGAGAGCGCGGTGACCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 613
 579 GCGCGCGCAGGCGCGGTGACCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 614

RESULT 10
 LOCUS HUMCALPS 2739 bp mRNA linear PRI 27-APR-1993
 DEFINITION Human calmodulin-like processed pseudogene, complete cds.
 ACCESSION M36707.1 GI:179878
 VERSION M36707.1
 KEYWORDS calmodulin; pseudogene.
 SOURCE Human leukocyte, CDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 2739)
 AUTHORS Koller M. and Strehler E.E.
 TITLE Characterization of an intronless human calmodulin-like pseudogene
 JOURNAL FEBS Lett. 239 (1), 121-128 (1988)
 MEDLINE 89031205
 PUBMED 3181418

FEATURES

source

Location/Qualifiers
 1. 2739
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_type="leukocyte"
 1066..1515
 /note="calmodulin-like pseudogene"
 /pseudo
 /codon_start=1

BASE COUNT 591 a 790 c 802 g 556 t
 ORIGIN

Query Match 24.6%; Score 211.2; DB 9; Length 2739;
 Best Local Similarity 64.7%; Pred. No. 4.5e-20;
 Matches 334; Conservative 0; Mismatches 173; Indels 9; Gaps 1;

107 CGCAGCATGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCCAGTACAAAAGGCTTCTC 166
 1059 CCTTGACATGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCCAGTACAAAAGGCTTCTC 1118
 167 CGCGTTGACAGGATGGAACGCAACATCAATGCGCGGTGAGCGCGCGCTGAA 226
 1119 CCTGTTGACAGGATGGAACGCAACATCAATGCGCGGTGAGCGCGCGCTGAA 1178
 227 GCGCAGGCGCAAGAACCTCTCGAGAGCGCGCAATGAGAAACATCTCCGAGCTTACAG 286
 1179 GTCCTGCGCGCAAGAACCTCTCGAGAGCGCGCAATGAGAAACATCTCCGAGCTTACAG 1238
 287 CGACGCGCAGGCGCAAGAACCTCTCGAGAGCGCGCAATGAGAAACATCTCCGAGCTTACAG 337
 1239 GACGCGCAGGCGCAGGCGCAAGAACCTCTCGAGAGCGCGCAATGAGAAACATCTCCGAGCTTACAG 1298
 338 GCGCAGGCGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCCAGTACAAAAGGCTTCTC 397
 1299 GACGCGCAGGCGCAGGCGCAAGAACCTCTCGAGAGAGAGCGCGCTTCCGCTGTTGACAGAGCGCA 1358
 398 GCGCAGGCGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 457
 1359 GCGCTTCTGACAGGCGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 1418
 458 GCGAGAGGAGCTGAGAGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 517
 1419 TGACGAGAGGAGCTGAGAGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 1478
 518 CTACGAGAGGAGCTGAGAGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 577
 1479 CTACGAGAGGAGCTGAGAGCGCGGTGACCTGACCTCCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 578
 578 GCTGCGCTGAGAGCGCGGTGACCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 613
 1539 GCGCGCGCAGGCGCGGTGACCTGAGAGAGAGCGCGCGCTTCCGCTGTTGACAGAGCGCA 1574

RESULT 11
 LOCUS AL732437 185926 bp DNA linear HTG 16-AUG-2002
 DEFINITION Homo sapiens chromosome 10 clone RP11-116G8, *** SEQUENCING IN
 ACCESSION AL732437
 VERSION AL732437.1 GI:22316190
 KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEPIN; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE Human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 185926)
 AUTHORS Bird C.
 TITLE Direct Submission
 JOURNAL Submitted (15-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk
 On Aug 19, 2002 this sequence version replaced gi:22204501.
 COMMENT ----- Genome Center

Db 1546 GGGCCCGACGGCCGACAGAGGAGAACCCGGGGC 1581

RESULT 13
HSCAMP5G 2746 bp DNA linear PRI 05-MAY-1993
LOCUS H.sapiens intronless calmodulin-like gene (CLP gene) for
DEFINITION calmodulin-like protein.
ACCESSION X13461
VERSION X13461.1 GI:29649
KEYWORDS calmodulin; calmodulin homologue.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2746)
AUTHORS Koller, M. and Strehler, E.E.
TITLE Characterization of an intronless human calmodulin-like pseudogene
JOURNAL FEBS Lett. 239 (1), 121-128 (1988)
MEDLINE 89031205
PUBMED 3181418

REFERENCE 2 (bases 1 to 2746)
AUTHORS Koller, M.
TITLE Direct Submission
JOURNAL Submitted (14-MAY-1990) Koller M., Swiss Federal Institute of
Technology, Laboratory for Biochemistry III, ETH Zentrum,
Universitaetsstr. 16, CH-8092 Zurich, Switzerland
revised by [3]

REFERENCE 3 (bases 1 to 2746)
AUTHORS Koller, M.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-1992)
REFERENCE 4 (bases 1 to 2746)
AUTHORS Koller, M. and Strehler, E.E.
TITLE Functional analysis of the promoters of the human CamIII calmodulin
gene and of the intronless gene coding for a calmodulin-like
protein
JOURNAL Blochim. Biophys. Acta 1163 (1), 1-9 (1993)
MEDLINE 93237314
PUBMED 8476923

FEATURES
SOURCE Location/Qualifiers
1..2746
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="lambda-hgH6"
/cell_type="leukocyte"
/tissue_type="blood"
misc_feature
813..820
/note="regulatory sequence"
promoter
892..896
/note="CAAT-box"
CDS
1073..1522
/note="high calmodulin-like protein"
/codon_start=1
/protein_id="CAA31809.1"
/db_xref="GI:29650"
/db_xref="SWISS-PROT:P27482"
/translation="MADQLTEEOYTEKEKAPSLFDKDGDCITTRRELQVNRSLGQNP
TEALRLDMMSIDKIDNGTVDFEFLCNMARKMDTNEEIRAFRFVFDKNGFVS
AAELRHVTRIGELTIDBEVDEMIRADTDGQVNEEFVRVLVSK"
misc_feature
2220..2225
/note="pot. polyA signal"
BASE COUNT 590 a 799 c 801 g 556 t
ORIGIN

Query Match 24.4%; Score 209.6; DB 9; Length 2746;
Best Local Similarity 64.5%; Pred. No. 7.5e-20;
Matches 333; Conservative 0; Mismatches 174; Indels 9; Gaps 1;

QY 107 CGCAGCATGCGCGGTGACCTCTGAGAGAGAGCCGACGATCAAAAAGCGTTTCTC 166
DB 1066 CCTGTGATGCGCGACGAGCTGACGAGAGAGGTCAAGAAATTCAGAGAGGCGCTCTC 1125

QY 167 CGCGGTGACAGGATGGAAGACGACCATCATGATCCCGAGAGCTGGCGGGCGGTGAA 226
DB 1126 CCTGTTTGACAAAGATGGGAGACGCTGATCAACACCGCGGAGCTGGGACGCTATCGC 1185

QY 227 GGCACAGGCGCAAGACCTTCGAGAGCCAGCTAAGAAATCATCTCCAGTTGACAG 286
DB 1186 GTCCCTGGGCGCAAGACCCAGGAGCGAGCTGGGGGACATGATGAGATGATGACCG 1245

QY 287 CGAGCGCGAGCGGAAATACGTCTCCAGAGTTCC-----TGACGCGCGCAAGCA 337
DB 1246 GCACGCGCAACGCGACCGGTGAGATCTCCGAGTTCTGGGCATGATGCGCAGAAATGAA 1305

QY 338 GGCAGAGGCGGCGCTGAGAGACCTGAGGTGCTTCGCGGCTTCGACACATGGCGA 397
DB 1306 GCACACGCGCAACGAGAGAGATCCGAGGCTTCGCGCTGTTGACACAGAGCGCA 1365

QY 398 CGGCACATCACCGTGGAGACCTCAGGCGGCGCATGGCGGGCTGGGGCAGCGCTGCC 457
DB 1366 CGGCTTCGTCAGCGCGCGCGGAGCTGCGACACTCATGACCCGCTGGGGAGAACTGAG 1425

QY 458 GCAGAGAGAGCTGAGACGCGCATATCCGCGAGGCCACGCTGACACAGAGAGCGGGGTGA 517
DB 1426 TGACAGAGAGAGTGGAGAGATATCCGGCCCGGACAGGAGAGAGAGAGAGGTGAA 1485

QY 518 CTACAGAGAGTTCGAGAGATGCTGCGCCAGAGAGTGGAGCTCCCGCTGTCCCGCTG 577
DB 1486 CTACAGAGAGTTCGCTGCTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1545

QY 578 GCTGCGCTCTGAGCTTCAGAGGCGCACCGCGCGCTGC 613
DB 1546 GGGCCCGACGGCGCCACAGAGGAGAACCCGGGGC 1581

RESULT 14
AC103443/C 106359 bp DNA linear HTG 12-JUL-2002
LOCUS Rattus norvegicus clone CH230-17869, *** SEQUENCING IN PROGRESS
DEFINITION *** 57 unordered pieces.
ACCESSION AC103443 GI:21728753
VERSION AC103443.3
KEYWORDS HTG; HTGS-PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 106359)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Albrooks, S.L., Amaralunge, H.C., Are, J.R., Ayala, M., Banks, T.,
Barbaric, J., Benton, J., Blinze, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P.,
Bunay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Devilla, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
DeLaney, K.R., Delgado, O., Dem, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earheart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frenzt, P.,
Gabriel, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B.,
Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsoun, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loutsegod, H.,
Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Me, J.,
Manshwar, M., Mapua, P., Martin, R., Martinale, A., Martinez, E.,
Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,

Miner, G., Miner, Z., Mitchell, T., Mohabhat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okunolu, G., Otaguaye, N., Ovielo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rotjokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shooshitari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Swalek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williamson, A., Wleciyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

Unpublished
2 (bases 1 to 106359)
Morley, K.C.

Submitted (25-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 106359)
Morley, K.C.

Direct Submission
Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:17973266.

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: GHOK
Center clone name: CH230-178G9

Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 53847 bases at least Q40
Consensus quality: 57227 bases at least Q30
Consensus quality: 60201 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 57 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1
1137: contig of 1137 bp in length
1138 1237: gap of unknown length
1238 2403: contig of 1166 bp in length
2404 2503: gap of unknown length
2503 3742: contig of 1239 bp in length
3742 3842: gap of unknown length
3842 5050: contig of 1208 bp in length
5050 5150: gap of unknown length
5150 6764: contig of 1614 bp in length
6764 6864: gap of unknown length
6864 7882: contig of 1018 bp in length
7882 9222: contig of 1240 bp in length
9222 9323: gap of unknown length
9323 10515: contig of 1193 bp in length
10515 10616: gap of unknown length
10616 12083: contig of 1468 bp in length

12084 12183: gap of unknown length
12184 13278: contig of 1095 bp in length
13278 13379: gap of unknown length
13379 14561: contig of 1183 bp in length
14561 14662: gap of unknown length
14662 15688: contig of 1027 bp in length
15688 15789: gap of unknown length
15789 16988: contig of 1199 bp in length
16988 17088: gap of unknown length
17088 18406: contig of 1318 bp in length
18406 18506: gap of unknown length
18506 19607: contig of 1101 bp in length
19607 19707: gap of unknown length
19707 20952: contig of 1246 bp in length
20952 21053: gap of unknown length
21053 22343: contig of 1291 bp in length
22343 22444: gap of unknown length
22444 24044: contig of 1600 bp in length
24044 24143: gap of unknown length
24143 25453: contig of 1309 bp in length
25453 25553: gap of unknown length
25553 27271: contig of 1718 bp in length
27271 27370: gap of unknown length
27370 27371: gap of unknown length
27371 28818: contig of 1448 bp in length
28818 28919: gap of unknown length
28919 30074: contig of 1155 bp in length
30074 30174: gap of unknown length
30174 32420: contig of 2246 bp in length
32420 32530: gap of unknown length
32530 33855: contig of 1335 bp in length
33855 33954: gap of unknown length
33954 35233: gap of unknown length
35233 35334: contig of 1279 bp in length
35334 35334: gap of unknown length
35334 36718: contig of 1385 bp in length
36718 36818: gap of unknown length
36818 38567: contig of 1749 bp in length
38567 38658: gap of unknown length
38658 40606: gap of unknown length
40606 40706: contig of 1939 bp in length
40706 42121: gap of unknown length
42121 42222: contig of 1415 bp in length
42222 43495: gap of unknown length
43495 43596: contig of 1274 bp in length
43596 43596: gap of unknown length
43596 45157: contig of 1562 bp in length
45157 45257: gap of unknown length
45257 46362: gap of unknown length
46362 46463: contig of 1105 bp in length
46463 47699: gap of unknown length
47699 47700: contig of 1237 bp in length
47700 47800: gap of unknown length
47800 49856: gap of unknown length
49856 49957: contig of 2057 bp in length
49957 51438: gap of unknown length
51438 51539: contig of 1482 bp in length
51539 53239: gap of unknown length
53239 53339: contig of 1701 bp in length
53339 55126: gap of unknown length
55126 55226: contig of 1787 bp in length
55226 55227: gap of unknown length
55227 56884: contig of 1658 bp in length
56884 56984: gap of unknown length
56984 58782: contig of 1798 bp in length
58782 58883: gap of unknown length
58883 60529: gap of unknown length
60529 60530: contig of 1647 bp in length
60530 60630: gap of unknown length
60630 62748: gap of unknown length
62748 62848: contig of 2119 bp in length
62848 64502: gap of unknown length
64502 64603: contig of 1654 bp in length
64603 66493: gap of unknown length
66493 66593: contig of 1890 bp in length
66593 68896: gap of unknown length
68896 71271: contig of 2304 bp in length
71271 71371: contig of 2275 bp in length
71371 71372: gap of unknown length

Query Match	Best Local Similarity	Matches	Conservative	Score	DB	Length
92 GCGAGGTGCAGAGACGACGAGCGATGCGGTTAGCTGACTCCTGAGAGAGAGAGCCAGCA	63.8%	298	0	185.4	DB 2	106359
83222 GCTTTGTACCGAGACACAGCGGCATCTCTCAGCGGTTTACTAAGAGACAGTGGCTGAGTT						
152 CAAAAAGGCTTTCTTCGCGGTTGACACGAGTGAAGAAACGACACCATCAATGCCAGAGCT						
83162 ACACCAAGCTTTCGATAGGTTGACACAGATTAAGATGGCCGATCAACGTCACGAACT						
212 GGGCGCGCGCTGAAAGGCCACGCGGACAGAACTCTTCGGAGGCCACGCTAAGAAACTCAT						
83102 TGGAACTCATTAAGAAAGCAGATGGGTAGAACATCCACAGAAAGAACTGAAGCTCTCAT						
272 CTCGAGGTTGACAGCGACGCGGAGGGAATCAAGCTTCCAGGATTCCTAGAGCC---						
83042 CTCGAGGTTGACAGCGACGCGGAGGAGTGGCGATGGCCATTAAGAAATTTTAAACGCGCAT						
329 GCGAAGAAAGGCGGCGGCTGAGAGACCTGACAGTGCCTTCGCGCCCTTGACCA						
82982 GGAGAAATTAAGAAAGGAGGAGGAGAGAGTGCAGGCTGTGTTCCGGGCTTTGACCA						
389 GGATGGCCACGCGCCATCACCCTGTGAGAGAGCTCAGCGGCGGACATGCGGGCTGGGCA						
82922 GAATGGTATGGTATCATCAGCATGAGAGAACTCAAGCAAGGCTTGTCCACATGGGTGA						
449 GCCCGTCCGCGAGAGAGCTGACGCCATGATTCGCGCGGCGGAGAGCTGACAGAGCG						
82862 GACCGTGTCCGAGGAGGAGCTGAATGACATGATCCGTGTGGCTGTAGCAGACCAAGATGG						
509 GCGGGTGAACACGAGAGATTGCGAGAGATGCTCCGCCAGAGTAG						
82802 GAAGGTGAACATATGAGAGTTCTGTAGAGTCTTCTCCGAGAGTAG						

RESULT 15

MPAM 1519 bp mRNA linear PLN 28-JAN-1995

LOCUS M.pyrifera mRNA for calmodulin.

DEFINITION X85091.1 GI:728608

VERSION X85091.1

KEYWORDS calmodulin; calmodulin gene.

SOURCE giant kelp.

ORGANISM Macrocystis pyrifera

Macrocystis pyrifera

Eukaryote; stramenopiles; Phaeophyceae; Lamnariales; Lessoniaceae.

REFERENCE 1 (bases 1 to 1519)

AUTHORS Love,J., Oliver,I.R. and Trewavas,A.J.

JOURNAL The nucleotide sequence of Macrocystis pyrifera calmodulin cDNA

REFERENCE Plant Physiol. 108, 1748-1748 (1995)

AUTHORS 2 (bases 1 to 1519)

Love,J.

Direct Submission

71372 72552: contig of 1181 bp in length

* 72553 72652: gap of unknown length

* 72653 74919: contig of 2267 bp in length

* 74920 75019: gap of unknown length

* 75020 76630: contig of 1611 bp in length

* 76631 76731 76730: gap of unknown length

* 76731 79024: contig of 2294 bp in length

* 79025 79124: gap of unknown length

* 79125 82070 82069: contig of 2945 bp in length

* 82070 82169: gap of unknown length

* 82170 84926: contig of 2757 bp in length

* 84927 85027 85026: gap of unknown length

* 85027 85677: contig of 2551 bp in length

* 85678 87677: gap of unknown length

* 87678 90185: contig of 2508 bp in length

* 90186 90285: gap of unknown length

* 90286 93277: contig of 2992 bp in length

```

JOURNAL Submitted (02-MAR-1995) J. Lowe, The Institute of Cell & Molecular Biology, The University of Edinburgh, King's Building, Mayfield Road, Edinburgh EH8 3JH, Scotland, UK
FEATURES source location/Qualifiers
    misc_feature . . . 1..1519 /organism="Macrocystis pyrifera"
    gene /db_xref="taxon:35122" /sex="Female" /dev_stage="gametophyte" 1..609 /note="re-arrangement" 695..1144 /gene="calmodulin" 695..1144 /gene="calmodulin" /codon_start=1 /product="calmodulin" /protein_id="CA59418.1" /db_xref="GI:728609" /db_xref="SPTRMBL:Q40302" /translation="MDQLTEQIJAERKAFSLFDKDSDGTTTKEIGTVRSIGNP TEALDIMEVDAVDNGITDPDFELPMARKMTDSEEEIIIEAFVPDKDGFIIS AAEIRHIMTNLGKLTDEVDDEMIREADIDGGINVEEVKKMMMAK"
    polyA_signal 1415..1420 1415..1468 1469..1487 /note="re-arrangement"
    misc_feature 1488..1519 /note="portion of the MCS of the cloning vector phuscript SK-"
BASE COUNT 400 a 469 c 367 g 283 t
ORIGIN
Query Match 21.1% Score 181.2; DB 8; Length 1519; Best Local Similarity 65.3%; Pred. No. 6.6e-16; Matches 286; Conservative 0; Mismatches 143; Indels 9; Gaps 1;
QY 113 CATGCCCGTGAGCTGCATCCTGTGAGGAGAGAGCCCATACAAAAAGCCTTCCTCCGCGT 172
DB 694 CATGGCTGATCAGTTTAGCACGAGAGACAGATCGTGAGTTCAAAGAGGCCCTTCAGCGTGT 753
QY 173 TGACAAGGATGAAGAAGGCAACCATTCAATGCCAGAGACTGGCGCGCGCTGAAGGCCAC 232
DB 754 CGAACAAAGACGGCATGGGACCATCACACCACAAAGAGCTGGGCACTGTGATGCGCTGTT 813
QY 233 GGCGAAGAACTCTCGAGAGGCCCACTTAAGAAAATCTCTCCGAGGTTGACAGGACAGG 292
DB 814 GGCGCAAGAACCCGACCTGAGGCGCGAGCTGCAGACATGATCAACAGAGTTGACGCTGACG 873
QY 293 CGAGCGGCAATACGCTTCACGAGATTCTGA-----CGCGCGCAAGAGGCCAG 343
DB 874 CAACGGCAACCATCGACTTCGCCGAGTTCTGACCATGATGGCGGGCAAGATGAAGGACAC 933
QY 344 GGCGGCGCTGAGAGACCTGCAGGTGCGCTTCGCGGCTTCGACACAGATGGCGACGGCCA 403
DB 934 GGACAGGAGAGGAGATCATCGAGGCTTCGAAAGTGTTCACAAAGACGCGCAAGGGTTT 993
QY 404 CATTACGTTGAGAGAGCTCAGGCGGGGCGATGCGGGGCTGGGGGAGAGCGCGCGCAGGA 463
DB 994 CATTTCGCGCGCCAGTTCGCCCACTATCATACCAACTGSGGCGAGAACTGTACCGACGA 1053
QY 464 GGAGCTGGAGACCCATGATCCCGAGGCGAGGATGGAGCAGAGGGGCGGTGAACATAAGA 523
DB 1054 GGAGGTGAGACATGATCCCGGAGGCGTGAACATGACAGCGGTGACGGCGAGATCACTAGA 1113
QY 524 GGAGTTCGCGAGGATGCT 541
DB 1114 GGAGTTCGTCMAAGATGAT 1131

```


GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2003, 17:07:16 ; Search time 278 Seconds
(without alignments)
6950.412 Million cell updates/sec

Title: US-10-031-403-2

Perfect score: 858

Sequence: 1 aatcccgatccctgcgcgc.....aggaactgcgcgattcccaaaa 858

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	858	100.0	858	22	AAF55621
2	846.4	98.6	955	23	ABK43613
3	846.4	98.4	920	22	AAI63855
4	843.6	98.3	884	22	AAI63933
5	843.6	98.3	884	22	AAI63933
6	843.6	98.3	884	23	ABK43908
7	811.4	94.6	853	21	AAA10473
8	441.4	51.4	497	21	AAF21853
9	272.8	31.8	330	21	AACT4951

10	211.2	24.6	1306	24	ABL65422
11	211.2	24.6	1306	24	ABL65524
12	211.2	24.6	1306	24	ABL67798
13	210.4	24.5	487	22	AAI93552
14	209.6	24.4	2746	24	ABL67803
15	170	19.8	564	21	AAO03838
16	169.2	19.7	739	23	ABL20145
17	169.2	19.7	1049	23	ABL20141
18	169	19.7	995	23	ABL14119
19	169	19.7	2175	24	ABK83767
20	169	19.7	2247	22	AAI44950
21	155.8	18.2	681	21	AAO10892
22	146.6	17.1	654	11	AAO04332
23	146.6	17.1	654	24	ABK63445
24	140.8	16.4	504	11	AAO04334
25	140.6	16.4	447	24	ABN83905
26	140.2	16.3	447	11	AAO04331
27	140	16.3	1251	24	ABN83907
28	138.4	16.1	462	9	AAH80188
29	137	16.0	1361	24	ABI99274
30	136	15.9	1129	21	AAFI4569
31	134.8	15.7	490	21	AAO40960
32	130.8	15.2	549	21	AAO43517
33	130.2	15.2	716	21	AAO38557
34	130.2	15.2	774	21	AAO44956
35	125.2	14.6	751	21	AAO39827
36	123.4	14.4	1161	24	ABL63305
37	123.4	14.4	1173	20	AAI90997
38	123.4	14.4	6710	20	AAI90998
39	122.6	14.3	1929	19	AAV58275
40	122.6	14.3	1929	19	AAV58277
41	122.6	14.3	1958	19	AAV58276
42	122.6	14.3	1971	19	AAV58278
43	122.4	14.3	457	21	AAO43954
44	121.4	14.1	632	23	ABL19275
45	121.4	14.1	2514	23	ABL19276

ALIGNMENTS

RESULT 1
ID AAF55621 standard; DNA; 858 BP.

AC AAF55621;

DT 29-MAY-2001 (first entry)

DE Nucleotide sequence of a human calmodulin-like skin protein.

XX Human; calmodulin-like skin protein; CLSP; epidermal differentiation;

KW calcium-mediated signal pathway; epidermal proliferation; dry skin;

KW hyperkeratosis; parakeratosis; psoriasis; ichthyosis; neoplasia;

KW skin aging; skin damage; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 114..554

FT FR2796646-A1.

PD 26-JAN-2001.

PF 23-JUL-1999; 99FR-0009615.

PR 23-JUL-1999; 99FR-0009615.

PA (ORF) L'OREAL SA.

XX

Lung cancer relate
Lung cancer relate
Oesophagus cancer
Human polynucleoti
Oesophagus cancer
Human secreted pro
Drosophila melanog
Drosophila melanog
Human cDNA diffe
cDNA encoding nove
Human secreted pro
Plasmid pRCM1 and
Rat sequence diffe
Plasmid pCAL7 con
Rat calmodulin enc
Recombinant calmod
Calcium sensor G85
DNA encoding biosy
Mouse ischaemic co
Aspergillus oryzae
Zea mays DNA fragm
Zea mays DNA fragm
Arabidopsis thailia
Arabidopsis thailia
Arabidopsis thailia
Breast cancer rela
Human centrin-2 ge
Human centrin-2 ge
Fluorescent calmod
Fluorescent calmod
Fluorescent calmod
Fluorescent calmod
Arabidopsis thailia
Drosophila melanog
Drosophila melanog

PI Mehul B, Bernard D, Simonetti L;
 DR WPI: 2001-184569/19.
 DR P-PSDB: AAB67650.
 XX
 PT New polypeptide isolated from human skin and having calcium fixing
 PT activity, useful for regulating epidermal proliferation and
 PT differentiation, e.g. in treatment of dry skin, psoriasis or neoplasia
 PT
 PS Claim 17: Page 22; 28pp; French.
 XX
 CC The present sequence encodes a human calmodulin-like skin protein
 CC (CLSP). CLSP is a calcium-mediated signal pathway modulator. CLSP
 CC polypeptides and polynucleotides are used cosmetically for regulating
 CC dysfunction of epidermal proliferation or differentiation (normal or
 CC pathological) and for treating dry skin, hyperkeratosis, parakeratosis,
 CC psoriasis, ichthyosis or neoplasia. They are especially used for
 CC treating skin aging and skin damage caused by exposure to ultraviolet
 CC radiation. They are also useful for preparing or purifying specific
 CC binding partners, especially specific antisera or monoclonal antibodies.
 CC
 XX
 SQ Sequence 858 BP; 155 A; 267 C; 301 G; 135 T; 0 other;
 Query Match 100.0%; Score 858; DB 22; Length 858;
 Best Local Similarity 100.0%; Pred. No. 8.6e-139;
 Matches 858; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 AATTCGCGGATCCCTGGCGGCTGCTGACACCTGACACGAGCTCTGAGACGAGGTT 60
 1 AATTCGCGGATCCCTGGCGGCTGCTGACACCTGACACGAGCTCTGAGACGAGGTT 60
 1 AATTCGCGGATCCCTGGCGGCTGCTGACACCTGACACGAGCTCTGAGACGAGGTT 60
 61 GAGGCGCGGTGGGAGCAGCTGCGAGGCTCCGAGAGTGACAGACGACGATGGCG 120
 61 GAGGCGCGGTGGGAGCAGCTGCGAGGCTCCGAGAGTGACAGACGACGATGGCG 120
 121 GTGAGTGAATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
 121 GTGAGTGAATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
 121 GTGAGTGAATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
 181 ATGGAACGCGACCATCATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 181 ATGGAACGCGACCATCATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 181 ATGGAACGCGACCATCATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 241 ACCTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 241 ACCTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 241 ACCTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 301 AATTCAGCTTCAGAGAGTCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 301 AATTCAGCTTCAGAGAGTCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 301 AATTCAGCTTCAGAGAGTCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 301 AATTCAGCTTCAGAGAGTCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 361 TGCAGGTGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
 361 TGCAGGTGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
 361 TGCAGGTGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
 421 TCAGGCGGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
 421 TCAGGCGGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
 421 TCAGGCGGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
 481 TCAGGCGGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
 481 TCAGGCGGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
 481 TCAGGCGGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
 541 TCAGGCGGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 541 TCAGGCGGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 541 TCAGGCGGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 601 CACCGCGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 601 CACCGCGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 601 CACCGCGCGCTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 661 AACTGCTCCCTCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720

DB 661 AACTGCTCCCTCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
 OY 721 CCGCGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 DB 721 CCGCGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 OY 781 GTCCCGCTTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 DB 781 GTCCCGCTTTCGCGGCTTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 OY 841 GACTGCGGAGTTCGAAA 858
 DB 841 GACTGCGGAGTTCGAAA 858
 RESULT 2
 ID ABR43613 standard; cDNA: 955 BP.
 AC ABR43613;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE DNA encoding novel central nervous system protein #193.
 XX
 KW Central nervous system; CNS; autoimmune disease; Rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 PN W020015318-A2.
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01332.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 23-AUG-2000; 2000US-0227182.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 05-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0233397.
 PR 14-SEP-2000; 2000US-0233398.
 PR 14-SEP-2000; 2000US-0233399.
 PR 14-SEP-2000; 2000US-0233400.
 PR 14-SEP-2000; 2000US-0233401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235835.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.

PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251858.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPL: 2001-581633/65.
 P-PSDB: AA087283.
 New isolated nucleic acid encoding a protein for diagnosing,
 preventing, treating or ameliorating medical conditions and used as
 food additives or preservatives -
 Claim 1; SEQ ID No 203; 837pp; English.
 The invention describes an isolated nucleic acid molecule (I) encoding a
 novel central nervous system protein..(I) and polypeptides (III) encoded
 by (I), are used to treat a medical conditions and in diagnosis of a
 pathological condition. Disorders which are diagnosed or treated include
 autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 anglogenesis, nervous system disorders e.g. Alzheimer's disease and
 amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
 adenocarcinomas and irritable bowel syndrome, reproductive system
 disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 leukaemia, disorders involving neovascularisation e.g. malignancies,
 respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 acute kidney failure and blood related disorders e.g. myocardial
 infarction. The polypeptides can also be used to aid wound healing and
 epithelial cell proliferation, to prevent skin aging due to sunburn, to
 maintain organs before transplantation, for supporting cell culture of
 primary tissues, to regenerate tissues and in chemotaxis. The
 polypeptides can also be used as a food additive or preservative to
 increase or decrease storage capabilities, fat content, lipid, protein,

RESULT3	
AA163855	
ID	AA163855 standard; cDNA: 920 BP
XX	
AC	AA163855;
XX	
DT	22-OCT-2001 (first entry)
XX	

DE	Human polynucleotide seq ID NO 63.
XX	Human; antiarrhythmic; antineumatic; antiproliferative; vasotropic;
KW	cardioprotective; nootropic; neuroprotective; antibacterial; virucide;
KW	fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW	neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW	antiflamatory; anticancer; vulnerary; anticonvulsant; antibacterial;
KW	antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW	cardiovascular disorder; neurological disease; infection; human; ss.
OS	
XX	Homo sapiens.
XX	
PN	WO200155308-A2.
XX	
PD	02-AUG-2001.
XX	
PF	17-JAN-2001; 2001WO-US01309.
XX	
XX	31-JAN-2000; 2000US-0179065.
PR	04-FEB-2000; 2000US-0180628.
PR	24-FEB-2000; 2000US-0184664.
PR	02-MAR-2000; 2000US-0186350.
PR	16-MAR-2000; 2000US-0198874.
PR	17-MAR-2000; 2000US-0199076.
PR	18-APR-2000; 2000US-0198123.
PR	19-MAY-2000; 2000US-0205515.
PR	07-JUN-2000; 2000US-0209467.
PR	28-JUN-2000; 2000US-0214886.
PR	30-JUN-2000; 2000US-0215135.
PR	07-JUL-2000; 2000US-0216647.
PR	07-JUL-2000; 2000US-0216886.
PR	11-JUL-2000; 2000US-0217487.
PR	11-JUL-2000; 2000US-0217496.
PR	14-JUL-2000; 2000US-0218290.
PR	26-JUL-2000; 2000US-0220963.
PR	26-JUL-2000; 2000US-0220964.
PR	14-AUG-2000; 2000US-0224518.
PR	14-AUG-2000; 2000US-0224519.
PR	14-AUG-2000; 2000US-0225213.
PR	14-AUG-2000; 2000US-0225214.
PR	14-AUG-2000; 2000US-0225266.
PR	14-AUG-2000; 2000US-0225267.
PR	14-AUG-2000; 2000US-0225268.
PR	14-AUG-2000; 2000US-0225270.
PR	14-AUG-2000; 2000US-0225447.
PR	14-AUG-2000; 2000US-0225757.
PR	14-AUG-2000; 2000US-0225758.
PR	14-AUG-2000; 2000US-0225759.
PR	18-AUG-2000; 2000US-0226279.
PR	22-AUG-2000; 2000US-0226681.
PR	22-AUG-2000; 2000US-0226868.
PR	22-AUG-2000; 2000US-0227182.
PR	23-AUG-2000; 2000US-0227009.
PR	30-AUG-2000; 2000US-0228924.
PR	01-SEP-2000; 2000US-0229287.
PR	01-SEP-2000; 2000US-0229343.
PR	01-SEP-2000; 2000US-0229344.
PR	01-SEP-2000; 2000US-0229345.
PR	05-SEP-2000; 2000US-0229509.
PR	05-SEP-2000; 2000US-0229509.
PR	06-SEP-2000; 2000US-0229513.
PR	06-SEP-2000; 2000US-0230437.
PR	08-SEP-2000; 2000US-0231242.
PR	08-SEP-2000; 2000US-0231243.
PR	08-SEP-2000; 2000US-0231244.
PR	08-SEP-2000; 2000US-0231413.
PR	08-SEP-2000; 2000US-0231414.
PR	08-SEP-2000; 2000US-0232080.
PR	12-SEP-2000; 2000US-0232081.
PR	14-SEP-2000; 2000US-0232397.
PR	14-SEP-2000; 2000US-0232398.
PR	14-SEP-2000; 2000US-0232399.

PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 25-SEP-2000; 2000US-0234999.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235835.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241281.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246539.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249267.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 01-DEC-2000; 2000US-0250300.
 PR 01-DEC-2000; 2000US-0250360.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.

PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251859.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI; 2001-488781/53.
 XX P-PSDB; AAM43549.
 PT New isolated nucleic acids and polypeptides, useful for diagnosing,
 PT treating and/or preventing human diseases and disorders -
 XX
 XX Claim 1; SEQ ID NO 63; 664bp + Sequence Listing; English.
 CC
 CC The invention relates to human polynucleotides (AAM434497-AAM43660) useful for preventing, treating
 CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. The
 CC genes were isolated from a range of human tissues disclosed in the
 CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
 CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
 CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
 CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
 CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 920 BP; 197 A; 274 C; 313 G; 135 T; 1 other;
 Query Match 98.4%; Score 844.4; DB 22; Length 920;
 Best Local Similarity 99.1%; Pred. No. 1.8e-136;
 Matches 848; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 3 TTCGCGATCCTCGGCGCTGCTGACATCTGACACGACGCTCTGAGACACAGGTTGA 62
 DB 26 TGCCCGGATCCTCGGCGCTGCTGACATCTGACACGACGCTCTGAGACACAGGTTGA 85
 QY 63 GGGCGCGTGGGAGCAGCTCGGAGGCTCGCGAGGTGACAGAGCAGCAGTGGCGGT 122
 DB 86 GGGCGCGTGGGAGCAGCTCGGAGGCTCGCGAGGTGACAGAGCAGCAGTGGCGGT 145
 QY 123 GAGCTGACTCTGAGAGGAGGCGCCAGTACAAAAGGCTTTCTCCGGTTGACACGAT 182
 DB 146 GAGCTGACTCTGAGAGGAGGCGCCAGTACAAAAGGCTTTCTCCGGTTGACACGAT 205
 QY 183 GGAAGGCGACCATCATATCCAGAGCTGGGCGGCGCTTAAGGCGACGGCAAGAC 242
 DB 206 GGAAGGCGACCATCATATCCAGAGCTGGGCGGCGCTTAAGGCGACGGCAAGAC 265
 QY 243 CTCTCGAGAGCGCAGTGAAGAACTCATCTCGAGGTTGACAGGAGCGAGCGCA 302
 DB 266 CTCTCGAGAGCGCAGTGAAGAACTCATCTCGAGGTTGACAGGAGCGAGCGCA 325
 QY 303 ATCAGCTTCAGAGTTCCTGACGCGGCGCAGAGAGCGCGCGCTTGAGAGCACTG 362
 DB 326 ATCAGCTTCAGAGTTCCTGACGCGGCGCAGAGAGCGCGCGCTTGAGAGCACTG 385
 QY 363 CAGGTGCGCTTCGCGCTTGCACAGAGTGGCGAGCGGCACATCAGCTGGACGACTC 422
 DB 386 CAGGTGCGCTTCGCGCTTGCACAGAGTGGCGAGCGGCACATCAGCTGGACGACTC 445

QY 423 AGCGGGCCATGCGGGGCTGTGGGAGCCGCTGCCGAGAGAGACTGAGCCCATGATC 482
DB 446 AGCGGGGCGATGCGGGGCTGTGGGAGCCGCTGCCGAGAGAGACTGAGCCCATGATC 505
QY 483 CGCGAGGCGGAGTGGACGAGAGCGGGGGTGAATCAGAGAGATTGGCAGATGCTC 542
DB 506 CGCGAGGCGGAGTGGACGAGAGCGGGGGTGAATCAGAGAGATTGGCAGATGCTC 565
QY 543 GCCCAGAGAGAGGCTCCCGGCTGTGTCGCCCTGGCTGCTGACCTTCAGAGGCA 602
DB 566 GCCCAGAGAGAGGCTCCCGGCTGTGTCGCCCTGGCTGCTGACCTTCAGAGGCA 625
QY 603 CGCGCGGCTGTGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 662
DB 626 CGCGCGGCTGTGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 685
QY 663 CTGCGCTCCCGCTGGAGAGAGGCTTTGGCTCCGGGGGCTGGATGGCGGCTCGGGCC 722
DB 686 CTGCGCTCCCGCTGGAGAGAGGCTTTGGCTCCGGGGGCTGGATGGCGGCTCGGGCC 745
QY 723 GCGTCGAGAGCCCTCTCTGCTTACAGACCTTGGGAGAGAGGCTCTTGGGCTGTGT 782
DB 746 GCGTCGAGAGCCCTCTCTGCTTACAGACCTTGGGAGAGAGGCTCTTGGGCTGTGT 805
QY 783 CCCCCCTTGGCCCTGACGTGAGATGAGGGCCCTTAACCCCGCATTTGATCTAATAAGGA 842
DB 806 CCCCCCTTGGCCCTGACGTGAGATGAGGGCCCTTAACCCCGCATTTGATCTAATAAGGA 865
QY 843 CTGCCGAGTTCCAAA 858
DB 866 CTGCCGAGTTCCAAA 881

RESULT 4
AA163933
ID AA163933 standard; cDNA; 884 BP.
XX AA163933;
AC
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 141.
XX
KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antitumor; antineoplastic; anticonvulsant; antibacterial;
KW antiparasitic; cardiac; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human; ss.
XX
OS Homo sapiens.
XX
PN WO20015308-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01309.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.

PR 20-OCT-2000; 2000US-0241825.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246533.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0250393.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PJ Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI: 2001-488781/53.
 DR P-PSDB: AAM43627.
 XX
 PT New isolated nucleic acids and polypeptides, useful for diagnosing,
 PT treating and/or preventing human diseases and disorders -
 XX
 PS Claim 1: SEQ ID NO 141; 664bp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AA163803-AA164012) and
 CC the encoded proteins (AAM44497-AAM43660) useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. The
 CC genes were isolated from a range of human tissues disclosed in the
 CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
 CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
 CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
 CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
 CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,

CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 884 BP; 162 A; 273 C; 311 G; 135 T; 3 other;

Query Match 98.3%; Score 843.6; DB 22; Length 884;

Best Local Similarity 98.8%; Pred. No. 2.5e-136;

Matches 846; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 3 TTCCCGATCCCTCGCGCTCCCTGCACATCTGGACACAGAGCTTGACAGCAGGTTGA 62
 DB 24 TGCCCGATCCCTCGCGCTCCCTGCACATCTGGACACAGAGCTTGACAGCAGGTTGA 83
 QY 63 GGGCCGGTGGGAGCAGCTCGAGGCTCCGCGAGGTGACAGAGCAGCAGCAGTGGCGGT 122
 DB 84 GGGCCGGTGGGAGCAGCTCGAGGCTCCGCGAGGTGACAGAGCAGCAGCAGTGGCGGT 143
 QY 123 GAGCTGACTCTGAGAGAGAGGCGCAGTACAAAAGCTTTCTCCGCGTTGACACGAT 182
 DB 144 GAGCTGACTCTGAGAGAGAGGCGCAGTACAAAAGCTTTCTCCGCGTTGACACGAT 203
 QY 183 GGAACAGCAGCAGTCAATGATCCGAGAGCTGGGCGGCGCTGAAGGCGACAGGCAAGAC 242
 DB 204 GGAACAGCAGCAGTCAATGATCCGAGAGCTGGGCGGCGCTGAAGGCGACAGGCAAGAC 263
 QY 243 CTCTCGAGAGCCAGCTAAGAAATCATCTCCGAGGTTGACAGCAGCAGGCGAGAA 302
 DB 264 CTCTCGAGAGCCAGCTAAGAAATCATCTCCGAGGTTGACAGCAGCAGGCGAGAA 323
 QY 303 ATCAGCTTCAGAGAGTTCTGAGCGGCGCAAGAAAGCCAGGCGCGCTGAGAGACTG 362
 DB 324 ATCAGCTTCAGAGAGTTCTGAGCGGCGCAAGAAAGCCAGGCGCGCTGAGAGACTG 383
 QY 363 CAGGTGCGCTTCGCGGCTTCGACAGAGATGGGAGCGGCACATCACTGAGAGAGCTC 422
 DB 384 CAGGTGCGCTTCGCGGCTTCGACAGAGATGGGAGCGGCACATCACTGAGAGAGCTC 443
 QY 423 AGCGGGGAGGAGGCGGGGTGGGAGCGGCTCCGAGAGAGAGTGGAGCGCATGATC 482
 DB 444 AGCGGGGAGGAGGCGGGGTGGGAGCGGCTCCGAGAGAGAGTGGAGCGCATGATC 503
 QY 483 CGGAGGCGGAGGTGAGCAGAGAGCGGGGGGTGAATACGAGAGATTCGCGAGATGCTC 542
 DB 504 CGGAGGCGGAGGTGAGCAGAGAGCGGGGGGTGAATACGAGAGATTCGCGAGATGCTC 563
 QY 543 GCCAGAGAGTGAAGGCTCCCGGCTGTGCTCCCTGGCTGGCTGAGGCTTGAAGGCCA 602
 DB 564 GCCAGAGAGTGAAGGCTCCCGGCTGTGCTCCCTGGCTGGCTGAGGCTTGAAGGCCA 623
 QY 603 CGCGCCGCTGCTCTTTTGTGTGGAGCTCCGCGGAAACCTGTGAGTGAAGGAA 662
 DB 624 CGCGCCGCTGCTCTTTTGTGTGGAGCTCCGCGGAAACCTGTGAGTGAAGGAA 683
 QY 663 CTGCTCTCCCTGGAGAGAAAGCTTTGCGCTCCGGGCGCTGATGCGGGCGCTCGGGCC 722
 DB 684 CTGCTCTCCCTGGAGAGAAAGCTTTGCGCTCCGGGCGCTGATGCGGGCGCTCGGGCC 743
 QY 723 GCTTGAGAGCCCTCTCTGCTTCACAGCTTGAGGAGAGAGAGGCTCTTGAGGCTGAT 782
 DB 744 GCTTGAGAGCCCTCTCTGCTTCACAGCTTGAGGAGAGAGAGGCTCTTGAGGCTGAT 803
 QY 783 CCGCTTTGCTGCTGAGTGAAGAGGCGCTTAAACCCGCAATGATTAATAAAGA 842
 DB 804 CCGCTTTGCTGCTGAGTGAAGAGGCGCTTAAACCCGCAATGATTAATAAAGA 863
 QY 843 CTGCGAGTTCAGAA 858
 DB 863

Db 864 CTGCCAGTCAAAA 879

RESULT 5
AAS31614
ID AAS31614 standard; cDNA; 884 BP.
XX
AC AAS31614;
XX
DT 04-DEC-2001 (first entry)
XX
DE cDNA encoding novel human calcium-binding protein #38.
XX
KW Human; calcium-binding protein; calcium flux; neurological disease;
KW immune dysfunction; digestive disorder; neoplastic disease;
KW blood disorder; infectious disease; gene therapy; immunosuppressive;
KW antithrombotic; cytostatic; vasotropic; antibacterial; nootropic;
KW vitruclide; ss.
XX
OS Homo sapiens.
XX
PN W0200155304-A2.
XX
PD 02-AUG-2001.
XX
PE 17-JAN-2001; 2001WO-US01302.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 23-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.

PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0235837.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241121.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.

PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 PI WPI: 2001-465568/50.
 XX P-PSDB: AAU19929.
 DR
 DR
 PT Isolated nucleic acid molecule encoding a calcium-binding protein is
 PT used in preventing, treating or ameliorating a medical condition -
 XX
 PS Claim 4; SEQ ID No 48; 542pp; English.
 XX
 XX The present invention relates to the isolation of novel human
 CC calcium-binding proteins (AAU19892-AAU19969), and cDNA and genomic
 CC sequences encoding for these proteins. The sequences of the invention
 CC are useful in the diagnosis, prevention and/or prognosis of diseases
 CC associated with aberrant calcium flux. Such disorders include
 CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
 CC immune dysfunction (e.g. severe combined immunodeficiency, SCID),
 CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
 CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
 CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
 CC novel calcium-binding proteins are also useful as screening tools to
 CC identify antagonists and/or agonists that may enhance or inhibit
 CC activities mediated by calcium-binding proteins. The polynucleotides of
 CC the invention are also useful in gene therapy. AAS31577-AAS31654
 CC represent cDNA sequences encoding for the novel human calcium-binding
 CC proteins.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 884 BP; 162 A; 273 C; 311 G; 135 T; 3 other:
 Query Match 98.3%; Score 843.6; DB 22; Length 884;
 Best Local Similarity 98.8%; Pred. No. 2.5e-136;
 Matches 846; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 0y 3 TTCCCGGATCCCTGGCGGCTGCGACTGACACGAGCTGTGAGAGCAGGTTGA 62
 Db 24 TCCCCGAGTCCCTGGCGGCTGCGACTGACACGAGCTGTGAGAGCAGGTTGA 83
 0y 63 GGGCCGCTGGGAGCAGCTCGAGGCTCCGCGAGGTGACGAGACCCAGCAGTGGCCGCT 122
 Db 84 GGGCCGCTGGGAGCAGCTCGAGGCTCCGCGAGGTGACGAGACCCAGCAGTGGCCGCT 143
 0y 123 GAGCTGACCTCTGAGAGAGAGGCCAGTCAAAAAGGCTTTCTCCGGGTGACAGCGAT 182
 Db 144 GAGCTGACCTCTGAGAGAGAGGCCAGTCAAAAAGGCTTTCTCCGGGTGACAGCGAT 203
 0y 183 GGAACGAGCAGCAGTCAATCCAGAGAGCTGGGCGGCGCTCAAGGCGACGAGCAAGAC 242
 Db 204 GGAACGAGCAGCAGTCAATCCAGAGAGCTGGGCGGCGCTCAAGGCGACGAGCAAGAC 263
 0y 243 CTCTCGAGAGGCCAGCTAAGAACTCATCTCCGAGGTTGACAGCGAGCGGCGAGAA 302

Db 264 CTCTCGAGAGGCCAGCTAAGAACTCATCTCCGAGGTTGACAGCGAGCGGCGAGAA 323
 0y 303 ATCAGCTTCCAGAGATTCTCTGACGGCGGCAAGAGAGCGGCGGCTGAGAGACTG 362
 Db 324 ATCAGCTTCCAGAGATTCTCTGACGGCGGCGAAGAGAGCGGCGGCTGAGAGACTG 383
 0y 363 CAGTGGCTTCCGCGGCTTCCGAGACAGAGATGGGAGAGCGGCAATCAACCGTGGACGCTC 422
 Db 384 CAGTGGCTTCCGCGGCTTCCGAGACAGAGATGGGAGAGCGGCAATCAACCGTGGACGCTC 443
 0y 423 AGGCGGCGCATGGCGGGGCTGGGCGAGCCGCTCCGAGAGAGAGCTGAGCGCATGATC 482
 Db 444 AGGCGGCGCATGGCGGGGCTGGGCGAGCCGCTCCGAGAGAGAGCTGAGCGCATGATC 503
 0y 483 CGGAGGCGCAGCTGACACAGAGAGCGGCGGTTAATCAGAGAGTTCGAGAGATGCTC 542
 Db 504 CGGAGGCGCAGCTGACACAGAGAGCGGCGGTTAATCAGAGAGTTCGAGAGATGCTC 563
 0y 543 GCCCAGAGTGAAGGCTCCCGGCTGTGTCCCTGGCTGCGCTGAGCCTCAGGGCCA 602
 Db 564 GCCCAGAGTGAAGGCTCCCGGCTGTGTCCCTGGCTGCGCTGAGCCTCAGGGCCA 623
 0y 603 CCGCCGCTGCTCTTTTGTGTGCTGGGACTCTCCGGGAAACCTGTGCTGATGGGAAA 662
 Db 624 CCGCCGCTGCTCTTTTGTGTGCTGGGACTCTCCGGGAAACCTGTGCTGATGGGAAA 683
 0y 663 CTGCTCTCCCTGGGAGAGAGGCTTTGCGCTCCGGGCGCTGATGCGGCGCTCGGCGC 722
 Db 684 CTGCTCTCCCTGGGAGAGAGGCTTTGCGCTCCGGGCGCTGATGCGGCGCTCGGCGC 743
 0y 723 GCTTGAGAGCCCTCTGCTGCTGCTGACACTTGGGAGAGAGAGCCCTCTGGGCGCTGT 782
 Db 744 GCTTGAGAGCCCTCTGCTGCTGCTGACACTTGGGAGAGAGAGCCCTCTGGGCGCTGT 803
 0y 783 CCCCCTTTGCTGACAGTGAATGAGGCGCCCTTAACCCCGCATTTGATTAATAAGA 842
 Db 804 CCCCCTTTGCTGACAGTGAATGAGGCGCCCTTAACCCCGCATTTGATTAATAAGA 863
 0y 843 CTGCGGAGTTCCAAA 858
 Db 864 CTGCGGAGTTCCAAA 879
 RESULT 6
 ID ABK43908 standard; cDNA: 884 BP.
 AC ABK43908;
 XX
 XX 05-JUN-2002 (first entry)
 XX
 XX
 XX DNA encoding novel central nervous system protein #488.
 DE
 XX
 XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; ischemia; angiodysplasia;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy; gene; ss.
 XX
 XX Homo sapiens.
 OS
 PN WO200155318-A2.
 XX
 XX 02-AUG-2001.
 PD
 XX 17-JAN-2001; 2001WO-US01332.
 PF
 XX

PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234397.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.

PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 12-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-581633/65.
P-PSDB; AA087578.

New isolated nucleic acid encoding a protein for diagnosing,
preventing, treating or ameliorating medical conditions and used as

PT food additives or preservatives -
 XX Claim 1; SEQ ID No 498; 837pp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule (I) encoding a
 CC novel central nervous system protein. (II) and polypeptides (III) encoded
 CC by (I), are used to treat a medical conditions and in diagnosis of a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angioneuromatosis, nervous system disorders e.g. Alzheimer's disease and
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
 CC adenocarcinomas and irritable bowel syndrome, reproductive system
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 CC leukaemia, disorders involving neovascularisation e.g. melaninancies,
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 CC acute kidney failure and blood related disorders e.g. myocardial
 CC infarction. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC

Query Match 98.3%; Score 843.6; DB 23; Length 884;
 Best Local Similarity 98.8%; Pred. No. 2.5e-136;
 Matches 846; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 3 TTCCCGATCCCTGGCGCTGCTGACATCTGGACACAGAGCTGTGAGAGCAGCAGGTGA 62
 Db 24 TGCCCGATCCCTGGCGCTGCTGACATCTGGACACAGAGCTGTGAGAGCAGCAGGTGA 83
 QY 63 GGGCCGTGGGACAGAGCTCGAGAGCTCCGCGAGGTGACAGAGCAGCAGCATGCCGT 122
 Db 84 GGGCCGTGGGACAGAGCTCGAGAGCTCCGCGAGGTGACAGAGCAGCAGCATGCCGT 143
 QY 123 GAGCTGATCCCTGAGAGAGGCGCAGTAAAGAGCTTCTCGCGGTATACAGCAT 182
 Db 144 GAGCTGATCCCTGAGAGAGGCGCAGTAAAGAGCTTCTCGCGGTATACAGCAT 203
 QY 183 GGAAGAGCAGCATATATGCGAGAGCTGGCGGCGCTGAAGAGCAGCGGCAAGAAC 242
 Db 204 GGAAGAGCAGCATATATGCGAGAGCTGGCGGCGCTGAAGAGCAGCGGCAAGAAC 263
 QY 243 CTCTCGAGAGCCAGCTAAGAACTATCTCGAGGTGACAGCAGCGGCGGCA 302
 Db 264 CTCTCGAGAGCCAGCTAAGAACTATCTCGAGGTGACAGCAGCGGCGGCA 323
 QY 303 ATCAGCTTCCAGAGATCTCTGAGCGGCGCAAGAGCGCGGCTGTGAGAGCATCTG 362
 Db 324 ATCAGCTTCCAGAGATCTCTGAGCGGCGCAAGAGCGCGGCTGTGAGAGCATCTG 383
 QY 363 CAGGTGCGCTTCCGCGCTTGCAGCAGAGTGGCAGCATATACCTGTGACAGAGCTC 422
 Db 384 CAGGTGCGCTTCCGCGCTTGCAGCAGAGTGGCAGCATATACCTGTGACAGAGCTC 443
 QY 423 AGGCGGCGCATATGCGGCGCTGCGGAGCGCTGCGCAGAGAGAGCTGTGAGCATATG 482
 Db 444 AGGCGGCGCATATGCGGCGCTGCGGAGCGCTGCGCAGAGAGAGCTGTGAGCATATG 503
 QY 483 GCGGAGCGCGAGCTGAGCAGAGCGGCGGTGAACTACGAGAGATCTGCGGAGATGCTC 542
 Db 504 GCGGAGCGCGAGCTGAGCAGAGCGGCGGTGAACTACGAGAGATCTGCGGAGATGCTC 563
 QY 543 GCGGAGAGTATGAGCTCCCGCGCTGTGCCCTGTGAGAGCTGTGAGAGCTTCAAGAGCA 602
 Db 564 GCGGAGAGTATGAGCTCCCGCGCTGTGCCCTGTGAGAGCTTCAAGAGCA 623
 QY 603 CCGCCGCTGCTGCTTTTGTGCTGGAGACTTCCGGGGAAGAACTGTGCTGGATGGGAAA 662

Db 624 CCGCCCGCTGCTGCTTTTGTGCTGGAGACTCCGGGGAAGAACTGTGATGGGAAA 683
 QY 663 CTGCTCCCGCTGGAGAGAGCTTTGGCTCCGGGCGCTGGATGGGCGCTCGGGCC 722
 Db 684 CTGCTCCCGCTGGAGAGAGCTTTGGCTCCGGGCGCTGGATGGGCGCTCGGGCC 743
 QY 723 GCGTCCGAGCGCGCTCTCTGCTTCCAGACCTTGGCGGAGAGAGCGCTCTGGCGCTGT 782
 Db 744 GCGTCCGAGCGCGCTCTCTGCTTCCAGACCTTGGCGGAGAGAGCGCTCTGGCGCTGT 803
 QY 783 CCGCTTTCCTGAGTGAAGTGAAGGCGCCCTTAACCCCGATTGATCTAATAAGGA 842
 Db 804 CCGCTTTCCTGAGTGAAGTGAAGGCGCCCTTAACCCCGATTGATCTAATAAGGA 863
 QY 843 CTGCGAGTCCAAA 858
 Db 864 CTGCGAGTTCAAA 879

RESULT 7
 ID AAA10473 standard; cDNA; 853 BP.
 AC AAA10473;
 XX 18-JUL-2000 (first entry)
 DT
 XX
 DE cDNA encoding human disease-associated calmodulin protein (DACP-1).
 XX
 KW Disease-associated calmodulin protein; DACP-1; human; EF-hand;
 KW detection; quantitation; diagnosis; cancer; immune disorder;
 KW reproductive disorder; gynaecological; gene therapy; ss.
 OS Homo sapiens.

Key Location/Qualifiers
 FH 121..561
 FT /*tag= a
 FT /product= "Human DACP-1"

US6046315-A.
 04-APR-2000.
 03-NOV-1997; 97US-0963409.
 PR 03-NOV-1997; 97US-0963409.
 PA (INCY-1) INCYTE PHARM INC.

Hillman J, Corley NC, Shah P;
 WPI: 2000-282708/24.
 DR P-PSDB: AAB7548.
 XX

New polynucleotide encoding a disease associated calmodulin protein
 (DACP-1) useful for diagnosing, preventing and treating cancer, immune
 disorders and reproductive disorders
 PT
 PT
 XX
 PS Claim 4; Fig 1A-C; 27pp; English.

This sequence represents cDNA encoding human disease-associated
 calmodulin protein (DACP-1). cDNA sequences encoding DACP-1 were
 CC initially isolated from a breast tumor cDNA library, this sequence
 CC being a consensus. Human DACP-1 has four EF-hand calcium-binding
 CC domains, and has chemical and structural homology with other calmodulin
 CC proteins from human, rat and plasmidum falciptarum. DACP-1 proteins and
 CC nucleotides are useful for the diagnosis, prevention, or treatment of
 CC cancers, immune disorders (e.g., AIDS) and reproductive disorders,
 CC including endometriosis. DACP-1 nucleotides are useful for detecting and
 CC quantitating gene expression in biopsied tissues in which expression of
 CC the protein may be correlated with a disease. Such a diagnostic assay may

QY 3 TTCCCGATCCCTGGCGCTGCTGCTGACACGAGCTTGTGAGACAGAGTTGA 62
 DB 25 TGCCCGGATCCCTGGCGCTGCTGCTGACACGAGCTTGTGAGACAGAGTTGA 84
 QY 63 GGGCCGGTGGGACGACGCTGGAGGCTCCGCGAGTGCAGAGACGCGAGCATGGCCGT 122
 DB 85 GGGCCGGTGGGACGACGCTGGAGGCTCCGCGAGTGCAGAGACGCGAGCATGGCCGT 144
 QY 123 GAGCTGACTCTGAGAGAGAGGCGCCAGTACAAAAGGCTTTCCCGGGTTGACAGGAT 182
 DB 145 GAGCTGACTCTGAGAGAGAGGCGCCAGTACAAAAGGCTTTCCCGGGTTGACAGGAT 204
 QY 183 GGAAGGCGACATCAATGCTCCGAGAGCTGGGCGCGCTGAGGCGACAGCAAGAAC 242
 DB 205 GGAAGGCGACATCAATGCTCCGAGAGCTGGGCGCGCTGAGGCGACAGCAAGAAC 264
 QY 243 CTCTCGAGGCGCCAGCTAAGAAATCTATCTCGAGGTTGACAGAGCGGCGAGAA 302
 DB 265 CTCTCGAGGCGCCAGCTAAGAAATCTATCTCGAGGTTGACAGAGCGGCGAGAA 324
 QY 303 ATCAGCTTCAGAGTCTCTGAGGCGGCAAGGCGGCGCGCTGAGAGAGCTG 362
 DB 325 ATCAGCTTCAGAGTCTCTGAGGCGGCAAGGCGGCGCGCTGAGAGAGCTG 384
 QY 363 CAGGTGCGCTTCGCGCTTCGACAGAGTGGCGAGCGGCACATCACTGAGAGCTG 422
 DB 385 CAGGTGCGCTTCGCGCTTCGACAGAGTGGCGAGCGGCACATCACTGAGAGCTG 444
 QY 423 AGGCGGCGCATGGCGGGCTGGGCGAGC 450
 DB 445 AGGCGGCGCATGGCGGGCTGGGCGAGC 472

RESULT 9

AACT4951
 ID AACT4951 standard; cDNA; 330 BP.

AC AACT4951;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORE506 polynucleotide sequence SEQ ID NO:1011.

XX Human: open reading frame; ORFX; detection: cytostatic; hepatotropic;
 KW vulnery; antiproliferative; antiparkinsonian; neurotrophic; hepatotropic;
 KW anticonvulsant; osteopathic; antidiabetic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antidiabetic;
 KW antiviral; antibacterial; antifungal; antineoplastic; antihypertensive;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive; ss.

XX Homo sapiens.

OS WO200058473-A2.

PN 05-OCT-2000.

PD 31-MAR-2000; 2000WO-US08621.

PF 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 05-APR-1999; 99US-0127728.

PR 30-MAR-2000; 2000US-0540763.

PA (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;
 PI WPI; 2000-602362/57.
 DR P-PDB; AAB40742.
 XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 PS Claim 5; Page 976; 5507pp; English.

CC AACT4446 to AACT7606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cyostatic; hepatotropic; vulnery;
 CC antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;
 CC osteopathic; anticonvulsant; antidiabetic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antineoplastic; antibacterial; antiviral; antifungal; antineoplastic;
 CC antihypertensive; antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antineoplastic disease, to enhance
 CC coagulation, to inhibit thrombosis, and as a contraceptive.

SQ Sequence 330 BP; 75 A; 94 C; 116 G; 45 T; 0 other;

Query Match 31.8%; Score 272.8; DB 21; Length 330;
 Best local Similarity 99.3%; Pred. No. 2.3e-38;

Matches 274; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTCCCGATCCCTGGCGCTGCTGCTGACACGAGCTTGTGAGACAGAGTTGA 62
 DB 55 TGCCCGGATCCCTGGCGCTGCTGCTGACACGAGCTTGTGAGACAGAGTTGA 114
 QY 63 GGGCCGGTGGGACGACGCTGGAGGCTCCGCGAGTGCAGAGACGAGCATGGCCGT 122
 DB 115 GGGCCGGTGGGACGACGCTGGAGGCTCCGCGAGTGCAGAGACGAGCATGGCCGT 174
 QY 123 GAGCTGACTCTGAGAGAGAGGCGCCAGTACAAAAGGCTTTCCCGGGTTGACAGGAT 182
 DB 175 GAGCTGACTCTGAGAGAGAGGCGCCAGTACAAAAGGCTTTCCCGGGTTGACAGGAT 234
 QY 183 GGAAGGCGACATCAATGCTCCGAGAGCTGGGCGCGCTGAGGCGACAGCAAGAAC 242
 DB 235 GGAAGGCGACATCAATGCTCCGAGAGCTGGGCGCGCTGAGGCGACAGCAAGAAC 294
 QY 243 CTCTCGAGGCGCCAGCTAAGAAATCTATCTCGAGGTTGACAGAGCGGCGAGAA 278
 DB 295 CTCTCGAGGCGCCAGCTAAGAAATCTATCTCGAGGTTGACAGAGCGGCGAGAA 330

RESULT 10

ABL65422
 ID ABL65422 standard; DNA; 1306 BP.

AC ABL65422;

DT 15-MAY-2002 (first entry)

DE Lung cancer related gene sequence SEQ ID NO:3759.

KW Human: cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

XX PD 13-DEC-2001.

XX PF 30-MAY-2001; 2001WO-US10838.

XX PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234567P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.

XX (AVAL-) AVALON PHARM.

PA XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI P1 Soppet DR, Weaver Z;

XX WPI: 2002-188264/24.

DR. Screening for anti-neoplastic agent involves exposing cells to a
chemical agent to be tested for anti-neoplastic activity, and
determining a change in expression of a gene of a signature gene set

XX Claim 1; SEQ ID 4861; 44pp; English.

XX The present invention describes a method (M1) for screening for an
anti-neoplastic agent. The method involves exposing cells to a chemical
agent to be tested for anti-neoplastic activity, determining a change in
expression of at least one gene (I) of a signature gene set, where (I)
comprises a sequence (S) selected from 8447 sequences (given in ABL6166
to ABL70110), or is at least 95% identical to (S), where a change in
expression is indicative of anti-neoplastic activity. (I) has cytoskeletal
activity and can be used in gene therapy. M1 can be used for screening
an anti-neoplastic agent, and can be used for producing a product which
is the data collected with respect to the anti-neoplastic agent as a
result of M1, and the data is sufficient to convey the chemical
structure and/or properties of the agent. M1 can be used in the

Query Match	24.68;	Score 211.2;	DB 24;	Length 1306;		
Best Local Similarity	64.78;	Pred. No. 8e-28;				
Matches 334;	Conservative	0;	Mismatches 173;	Indels 9; Gaps		
OY	107	CGCGGCATGGCCGCTGAGCTGACTCCTTGAGGAGGCCACAGTACAAAAGGCTTCTC	166			
DB	119	CCCTGGCATGCCGACCAAGCTGACTGAGGAGGACAGTACAGAAATTAAAGAGGCTTCTC	178			
OY	167	CGCGGTTAGACAGGATGAAAGCGCACATCAATTGCCAGAGAGCTGGGCGGCGCTGAA	226			
DB	179	CCTGTTAGAAAGATGGGAGCGCTGCATCACACCCGCGAGCTGGGCGGCTGATGCG	238			
OY	227	GGCCAGGGGCAAGAACTCTCGGAGGCGCCAGCTTAAGAAACATCATCTCGAGGTTGACG	286			
DB	239	GTCCTTGAGGCAAGAACCCACAGAGGCGGAGCTGCGGAGACATGATAGTAGATGACCG	298			
OY	287	CGAGCGGAGCGCGCAAAATCAGCTTCCAGAGATTCC-----TGACGGCGGCAAGAA	337			
DB	299	GGAGGGCAAGGCAACGCTGAGACTTCCCGAGTTCTGAGGATATGAGCCAGAAATGAA	358			
OY	338	GGCCAGGCGCGGCTTGAGAGACTGACAGTCCGCTTCCGCGCTTGACAGAGATGGCA	397			
DB	359	GGACACGAGCAACAGGAGGAGATCCCGGAGGCTTCCGCGTGTGTGACAAAGACGCA	418			
OY	398	CGGCGACATCACCGTGGAGAGCTCAAGCGCGGCGCTGAGCGGGCTGGGGCAGCGCTGC	457			
DB	419	CGGCTTGTGTCAGCGCCCGCCAGCTACGACAGTCAATGACCCGGCTGGGGAGAACTGAG	478			
OY	458	GCAGGAGAGCTGGAGCGCATGATCCGCGAGCGCCAGTGGAGACAGAGCGGGCGGTGA	517			
DB	479	TGACGAGAGAGGTGAGCAGATGATCCCGGCGCGGACACGAGAGGAGAGGAGGTGA	538			
OY	518	CTACGAGGAGTTCGCGAGGATGCTCGCGCCACAGGAGTGGGCTCCCGCTGTGCCCCCTG	577			
DB	539	CTACGAGGAGTTCGCGGTGCTGCTGTGTCGTAAGTGAAGCGCGGCGCCACATGCTCTG	598			
OY	578	GCTCGCTCTGAGGCTTCAGGCGCACCGCCCGCTGC	613			
DB	599	GGCGCCACGCGGCCACAGGCGCAAGAACCCGGGCG	634			
RESULT 12						
ABL67798	standard; DNA; 1306 BP.					
AC	ABL67798;					
XX	15-MAY-2002	(first entry)				
DT	Oesophagus cancer related gene sequence SEQ ID NO:6135.					
XX	DE	XX				
XX	DE	XX				
XX	DE	XX				
KM	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;					
KM	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;					
KM	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;					
KM	gene; ds.					
OS	Homo sapiens.					
XX	MO200194629-A2.					
XX	13-DEC-2001.					
XX	30-MAY-2001;	2001MO-US10838.				
XX	05-JUN-2000;	2000US-209473P.				
XX						

PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-233133P.
 PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 20-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 PA (AVAL-) AVALON PHARM.
 XX
 XX
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX
 XX WPI: 2002-188264/24.
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set -
 XX
 XX
 PS Claim 1; SEQ ID 6135; 44pp; English.
 XX
 CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cyclostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilm's tumour.
 XX

SO Sequence 1306 BP; 258 A; 434 C; 403 G; 211 T; 0 other:
 Query Match 24.6%; Score 211.2; DB 24; Length 1306;
 Best Local Similarity 64.7%; Pred. No. 8e-28;
 Matches 334; Conservative 0; Mismatches 173; Indels 9; Gaps 1;
 QY 107 CGCAGGATGGCCGGTGAAGTCTGCTGCTGAGAGAGAGCCAGTCAAAAAGCTTCTC 166
 DB 119 CCCTGGCATGGCCGACACGACTGAGGACAGTCAAGAAATCAAGAGGCTTCTC 178
 QY 167 CGCGTTGACACGATGTAAGAACGACCATCAATGCCAGAGAGTGGCGGGCTTCTC 226
 DB 179 CCTGTTACAAAGATGGAGCGGCTGCTGATCAACCCGCACTGGGACGCTCATCG 238
 QY 227 GGCACAGGGCAAGAAGCTCTGAGAGCCAGCTAAGAAACTCATCTCGAGTTGACAG 286
 DB 239 GTCCCTGGCCAGAACCCACGAGGCGGAGCTGGGACATGATGATGATGACCG 298
 QY 287 CGACGGGACGCGCAAAATCAGCTTCCAGAGATTCC-----TGACGGGCGCAAGGA 337
 DB 299 GGACGGCAACGCGACCGGTGACTTCCGAGTCTGGGCATGATGGCCAGGAAGATGA 358
 QY 338 GGCCAGGCGCGGCTGAGAGACTGCAAGTGCCTTCGCGCTTCGACAGATGGGA 397
 DB 359 GGACAGCGACAAACGAGAGAGATCCCGGAGGCTTCCGCTGTTCCAGAAAGAGCGCA 418
 QY 398 CGGCCACATCACCGTGAAGCTGAGCGGCGGAGGCGGAGGCTGGGCGCGCTGCC 457
 DB 419 CGGCTTGCTGACGCGCGCGGCTGACGACATGCTACGCGCGGGGAGAGCTGAG 478
 QY 458 GCAGGAGAGCTGAGCGCATGATCCCGGAGCGGAGCTGACCAAGAGCGCGGTGA 517
 DB 479 TGACGAGAGGTGAGCAGATATCCGCGGCGGACAGCAGAGACAGACAGTGA 538
 QY 518 CTACGAGAGTTCGCGAGGATGCTGCCAGAGAGTGAAGCTCCCGCTGTCCTCTG 577
 DB 539 CTAGAGAGAGTTTCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 598
 QY 578 GCTGCGCTGAGCTTCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 613
 DB 599 GCGCGCCACGCGGCCACAGAGGCGGCAAGAACCGGGGCG 634
 RESULT 13
 AA193552
 ID AA193552 standard; cDNA; 487 BP.
 XX
 XX
 AC AA193552;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 13612.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation; ss.
 OS Homo sapiens.
 PN W0200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Dimaenac RT;

DR WPI: 2001-514838/56.
DR P-PSDB: AAO13621.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 1; SEQ ID NO 13612; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcr_sequences.
XX
SQ Sequence 487 BP; 130 A; 104 C; 128 G; 105 T; 20 other:

Query Match 24.5%; Score 210.4; DB 22; Length 487;
Best Local Similarity 96.4%; Pred. No. 1.2e-27;
Matches 214; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 637 GGGAAACCTGCTGGTGGATGGAACCTGCTCCCTGGAGAGAGGCTTGGCGTCG 696
DB 36 GGAATTCCTGCTGGTGGATGGAACCTGCTCCCTGGAGAGAGGCTTGGCGTCG 95
OY 697 GGGCTGATGG 756
DB 96 GGGCTGATGG 155
OY 757 CAGAAGAGAGGCTCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 816
DB 156 CAGAAGAGAGGCTCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 215
OY 817 AACCCCGCATGATCTAAATTAAGAGCTGCCAGATTCACAAA 858
DB 216 AACCCCGCATGATCTAAATTAAGAGCTGCCAGATTCACAAA 257

RESULT 14
ABL67803
ID ABL67803 standard; DNA; 2746 BP.
XX
AC ABL67803;
XX
DE 15-MAY-2002 (first entry)
XX
DE Oesophagus cancer related gene sequence SEQ ID NO:6140.
XX
DE Human: cancer: colon; breast; ovary; oesophagus; kidney; thyroid;
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
XX
PR 05-JUN-2000; 2000US-209531P.
XX
PR 18-SEP-2000; 2000US-233133P.

PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
XX (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX Soppet DR, Weaver Z;
XX
XX WPI: 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a
XX chemical agent to be tested for anti-neoplastic activity, and
XX determining a change in expression of a gene of a signature gene set -
XX
PS Claim 1; SEQ ID 6140; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an
XX anti-neoplastic agent. The method involves exposing cells to a chemical
XX agent to be tested for anti-neoplastic activity, determining a change in
XX expression of at least one gene (I) of a signature gene set, where (I)
XX comprises a sequence (S) selected from 8447 sequences (given in ABL61664
XX to ABL70110), or is at least 95% identical to (S), where a change in
XX expression is indicative of anti-neoplastic activity. (I) has cytoskeletal
XX activity and can be used in gene therapy. M1 can be used for screening
XX an anti-neoplastic agent, and can be used for producing a product which
XX is the data collected with respect to the anti-neoplastic agent as a
XX result of M1, and the data is sufficient to convey the chemical
XX structure and/or properties of the agent. M1 can be used in the
XX treatment of cancer such as colon, breast, stomach, lung, thyroid,
XX oesophageal, ovarian, kidney, prostate or pancreatic cancer,
XX adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
XX infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
XX carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ Sequence 2746 BP; 590 A; 799 C; 801 G; 556 T; 0 other;

GenCore version 5.1.4 p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 16, 2003, 03:47:16 ; Search time 58 Seconds
(without alignments)
771.979 Million cell updates/sec

Title: US-10-031-403-1
Perfect score: 729
Sequence: 1 MAGELTPEEEAQQYKAFSAV.....DVDGDGRVNYEFARMLAQE 146

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPRO.spool/US10031403/unat_08052003.131925.5712/app.query.fasta_1.327
-DB=Issued_Patents.NA -OPMT=fastacp -SUFFIX=rni -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=dits -START=1 -END=1 -MATRIX=Diosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pcp -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10031403 ECGN.1.1.40.0@unat.08052003.131925.5712 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMCOUT=120
-WARN_TIMCOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents.NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCNUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	726	99.6	853	3	US-08-963-409-2
2	376.5	51.6	1929	2	Sequence 2, Appl1
3	376.5	51.6	1929	4	Sequence 1, Appl1
4	376.5	51.6	1929	2	Sequence 1, Appl1
5	376.5	51.6	1929	2	Sequence 1, Appl1
6	376.5	51.6	1929	4	Sequence 3, Appl1
7	373.5	51.2	1929	2	Sequence 3, Appl1
8	373.5	51.2	1929	4	Sequence 5, Appl1
9	373.5	51.2	1971	2	Sequence 7, Appl1
10	355.5	48.8	906	4	Sequence 7, Appl1
11	324.5	44.5	1401	4	Sequence 1, Appl1
12	305.5	41.9	916	4	Sequence 3, Appl1

13	286.5	39.3	1173	4	US-09-285-601-1	Sequence 1, Appl1
14	286.5	39.3	6709	2	US-09-285-601-3	Sequence 3, Appl1
15	254	34.8	836	4	US-08-698-805-7	Sequence 7, Appl1
16	239.5	32.9	1173	3	US-08-993-380-3	Sequence 3, Appl1
17	237.5	32.6	1349	1	US-07-951-715A-20	Sequence 20, Appl1
18	237.5	32.6	1349	2	US-08-459-448A-20	Sequence 20, Appl1
19	237.5	32.6	1349	3	US-08-459-595A-20	Sequence 20, Appl1
20	237.5	32.6	1349	3	US-08-459-504B-20	Sequence 20, Appl1
21	237.5	32.6	1349	3	US-08-459-444-20	Sequence 0, Appl1
22	237.5	32.6	1349	4	US-09-547-422-20	Sequence 0, Appl1
23	201.5	27.6	704	3	US-09-048-889-7	Sequence 7, Appl1
24	191	26.2	1400	1	US-08-464-164-1	Sequence 1, Appl1
25	191	26.2	1400	1	US-08-338-057-1	Sequence 1, Appl1
26	191	26.2	1400	2	US-08-668-416-1	Sequence 1, Appl1
27	171.5	23.5	944	1	US-08-468-855-3	Sequence 3, Appl1
28	171.5	23.5	944	1	US-08-468-855-3	Sequence 3, Appl1
29	171.5	23.5	944	1	US-08-310-357-3	Sequence 3, Appl1
30	171.5	23.5	944	1	US-08-468-852-3	Sequence 3, Appl1
31	171.5	23.5	944	2	US-08-468-857-3	Sequence 3, Appl1
32	158.5	21.7	839	1	US-08-884-682-2	Sequence 2, Appl1
33	158.5	21.7	839	2	US-09-096-082-2	Sequence 2, Appl1
34	156	21.4	524	1	US-08-328-322-16	Sequence 16, Appl1
35	156	21.4	812	1	US-08-328-322-13	Sequence 13, Appl1
36	151	20.7	420	4	US-09-641-638-584	Sequence 229, App
37	144	19.8	463	4	US-09-641-638-234	Sequence 584, App
38	144	19.8	464	4	US-09-641-638-234	Sequence 234, App
39	144	19.8	464	4	US-09-641-638-235	Sequence 235, App
40	138.5	19.0	439	4	US-09-641-638-240	Sequence 240, App
41	138.5	19.0	611	4	US-09-328-111-527	Sequence 527, App
42	138	18.9	420	4	US-09-641-638-227	Sequence 227, App
43	136.5	18.7	439	4	US-09-641-638-241	Sequence 241, App
44	136.5	18.7	439	4	US-09-641-638-242	Sequence 242, App
45	124	17.0	1055	2	US-08-828-242-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-963-409-2
; Sequence 2, Application US/08963409
; Patent No. 6046315
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: DISEASE ASSOCIATED CALMODULIN PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,409
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0418 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 853 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: BRSTU14
 CLONE: 2743380
 US-08-963-409-2

Alignment Scores:

Pred. No.: 2,62e-81 Length: 853
 Score: 726.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.32% Mismatches: 0
 Query Match: 99.59% Indels: 0
 Gaps: 3

US-10-031-403-1 (1-146) x US-08-963-409-2 (1-853)

QY 1 MetAlaGlyLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
 Db 121 ATGGCCGAGTACGCTGCTGAGAGAGAGGCCAGTACAAAAGGCTTCTCCGCGGT 180
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleuLysAlaThr 40
 Db 181 GACACGATGGAAGGCGACCATCATGCCAGAGCTGGGGCGGCTGAAGGCCACG 240
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 241 GGCAAGAACTCTCGAGGGCCAGCTAAGAACTCATCTCCGAGGTGACAGCGAGCGC 300
 QY 61 AspGlyLeuIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
 Db 301 GACGGCCAAATCAAGCTTCCAGAGTTCTGACGGCGCGAAGGCCAGCGCGGCGCTG 360
 QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyHisIleThrVal 100
 Db 361 GAGGACCTGCAAGTGGCTTCCGCGCTTGCACAGAGTGGCGGCCCATCATCACCGTG 420
 QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluLeuAsp 120
 Db 421 GAGGAGCTCAGGGGGCGGCAATGAGGGGCTGGGGAGCGCTGCCGCGAGAGAGCTGGAC 480
 QY 121 AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGluIlePheAla 140
 Db 481 GCATGATCCGCGAGCGGCGAGCTGGACAGAGCGGGGCTGAACCTACGAGAGTTGCGC 540
 QY 141 ArgMetLeuAlaGlnGlu 146
 Db 541 AGGATGCTCCGCCAGAG 558

RESULT 2

US-08-818-253-1
 ; Sequence 1, Application US/08818253
 ; Patent No. 5998204

GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.
 TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESS: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/818,253
 FILING DATE: 14-MAR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Ph.D., Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07257/043001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1929 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

FEATURE: NAME/KEY: Coding Sequence

US-08-818-253-1

LOCATION: 1..1926

Alignment Scores:

Pred. No.: 1.97e-37 Length: 1929
 Score: 376.50 Matches: 75
 Percent Similarity: 73.29% Conservative: 32
 Best Local Similarity: 51.37% Mismatches: 36
 Query Match: 51.65% Indels: 3
 Gaps: 2

US-10-031-403-1 (1-146) x US-08-818-253-1 (1-1929)

QY 1 MetAlaGlyLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
 Db 688 ATGATGACCAACATGAGAGAGACAGATTCAGAGTTCAAAAGGCTTCTCATTTATTC 747
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleuLysAlaThr 40
 Db 748 GACAAGATGAGGCGGCGACCATCATCCCAAGAACTTGGCACCGTTATGAGTCTT 807
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 808 GCAAAACCAACCAAGCAGCAAGCAATTCAGAGATGATGATCAATGAAGTGCATGAGC 867
 QY 61 AspGlyLeuIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArg----- 77
 Db 868 AATGGAAGATTTACTTCTGAAATTTCTTACTATGATGCTGAAATAATGAAGACACA 927
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyHis 97
 Db 928 GACAGCGAAGAGAAATCCGAGAAAGCATTCGTTTTCACAAAGATGGGAAGCGCTAC 987
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
 Db 988 ATCAGCCCTCTGAAATTAATCTACATGATGACAAACCTCGGGGGAAGTTAACAGATGAA 1047
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGlu 137
 Db 1048 GAACTGATGAATGATTAAGGAGACGATATGATGATGATGATGATGATGATGATGATGAA 1107
 QY 138 GluPheAlaArgMetLeu 143
 Db 1108 GAGTTTGTACAAATGATG 1125

RESULT 3

US-08-818-252-1
 ; Sequence 1, Application US/08818252B
 ; Patent No. 6197928
 ; GENERAL INFORMATION:

: APPLICANT: Tsien, Roger Y.
 : TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
 : TITLE OF INVENTION: DETECTION OF ANALYTES
 : FILE REFERENCE: 07257/042001
 : CURRENT APPLICATION NUMBER: US/08/818, 2528
 : CURRENT FILING DATE: 1997-03-14
 : NUMBER OF SEQ ID NOS: 56
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO: 1
 : LENGTH: 1929
 : TYPE: DNA
 : ORGANISM: Aequorea victoria
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (0)...(1926)
 : US-08-818-252-1

Alignment Scores:
 Pred. No.: 1,97e-37 Length: 1929
 Score: 376.50 Matches: 75
 Percent Similarity: 73.29% Conservative: 32
 Best Local Similarity: 51.37% Mismatches: 36
 Query Match: 51.65% Indels: 3
 Gaps: 2

US-10-031-403-1 (1-146) x US-08-818-252-1 (1-1929)

QY 1 MetAlaGlyLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
 Db 688 ATGATGACGACCACTGACAGAGATTCAGAGATTCAAGAACCTTCATTATTC 747
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 Db 748 GACAAGATGGGGAGCGACCATCCACCAAGAACTTGGACCGTTATGAGTCGCTT 807
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 808 GGACAAACCCCAACGACGACGAAATTCAGATGATCAATGAAGTCGATCGATGCG 867
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 Db 868 AATGGAACGATTACTTCTGTAATTTCTTACTATGATGCGTGAAGAAATGAAGACACA 927
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAsnHis 97
 Db 928 GACAGCGAAGAGAAATCCGAGAACGATTCCTGTTTTCACAAAGATGGGAACGCTAC 987
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
 Db 988 ATCAGCCGCTGCTGAATTCACGTCACGTCATGACAAACCTCGGGGAGAACTTACAGATGAA 1047
 QY 118 GluLeuAspAlaMetIleArgGlnAlaAspValAspGlnAspGlyArgValAsnTyrGlu 137
 Db 1048 GAAGTTGATGAATGATATAGAGAACAGATATGATGATGATGCGCAAGTAAACTATGAA 1107
 QY 138 GluPheAlaArgMetLeu 143
 Db 1108 GAGTTTGTACAAATGATG 1125

RESULT 4
 : US-08-818-253-3
 : Sequence 3, Application US/08818253
 : Patent No. 5998204
 : GENERAL INFORMATION:
 : APPLICANT: Tsien, Roger Y.
 : APPLICANT: Miyawaki, Atsushi
 : TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
 : TITLE OF INVENTION: DETECTION OF ANALYTES
 : NUMBER OF SEQUENCES: 61
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Fish & Richardson P.C.
 : STREET: 4225 Executive Square, Suite 1400

: CITY: La Jolla
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 92037
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: Windows 95
 : SOFTWARE: FastSeq for Windows Version 2.0b
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/818, 253
 : FILING DATE: 14-MAR-1997
 : PRIORITY APPLICATION DATA:
 : APPLICATION NUMBER:
 : FILING DATE:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Halle, Ph.D., Lisa A.
 : REGISTRATION NUMBER: 38,347
 : REFERENCE/DOCKET NUMBER: 07257/043001
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 619/678-5070
 : TELEFAX: 619/678-5099
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1959 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: CDNA
 : FEATURE:
 : NAME/KEY: Coding Sequence
 : LOCATION: 1...1956
 : US-08-818-253-3

Alignment Scores:
 Pred. No.: 2.01e-37 Length: 1959
 Score: 376.50 Matches: 75
 Percent Similarity: 73.29% Conservative: 32
 Best Local Similarity: 51.37% Mismatches: 36
 Query Match: 51.65% Indels: 3
 Gaps: 2

US-10-031-403-1 (1-146) x US-08-818-253-3 (1-1959)

QY 1 MetAlaGlyLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
 Db 688 ATGATGACCACTGACAGAGATTCAGAGATTCAAGAACCTTCATTATTC 747
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 Db 748 GACAAGATGGGGAGCGACCATCCACCAAGAACTTGGACCGTTATGAGTCGCTT 807
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 808 GGACAAACCCCAACGACGACGAAATTCAGATGATCAATGAAGTCGATCGATGCG 867
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 Db 868 AATGGAACGATTACTTCTGTAATTTCTTACTATGATGCGTGAAGAAATGAAGACACA 927
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAsnHis 97
 Db 928 GACAGCGAAGAGAAATCCGAGAACGATTCCTGTTTTCACAAAGATGGGAACGCTAC 987
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
 Db 988 ATCAGCCGCTGCTGAATTCACGTCACGTCATGACAAACCTCGGGGAGAACTTACAGATGAA 1047
 QY 118 GluLeuAspAlaMetIleArgGlnAlaAspValAspGlnAspGlyArgValAsnTyrGlu 137
 Db 1048 GAAGTTGATGAATGATATAGAGAACAGATATGATGATGATGCGCAAGTAAACTATGAA 1107
 QY 138 GluPheAlaArgMetLeu 143

Db 1108 GAGTTGTACAAATGATG 1125
 RESULT 5
 US-08-818-252-3
 ; Sequence 3, Application US/08818252B
 ; Patent No. 6197928
 ; GENERAL INFORMATION:
 ; APPLICANT: Tsien, Roger Y.
 ; APPLICANT: Miyawaki, Atsushi
 ; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
 ; TITLE OF INVENTION: DETECTION OF ANALYTES
 ; FILE REFERENCE: 07257/042001
 ; CURRENT APPLICATION NUMBER: US/08/818, 252B
 ; CURRENT FILING DATE: 1997-03-14
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1959
 ; TYPE: DNA
 ; ORGANISM: Aequorea victoria
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (0)...(1956)
 US-08-818-252-3

Alignment Scores:
 Pred. No.: 2.01e-37 Length: 1959
 Score: 376.50 Matches: 75
 Percent Similarity: 73.29% Conservative: 32
 Best Local Similarity: 51.37% Mismatches: 36
 Query Match: 51.65% Indels: 3
 Gaps: 2

US-10-031-403-1 (1-146) x US-08-818-252-3 (1-1959)

Qy 1 MetAlaGlyLeuThrProGluGluAlaGlnTyrIleuValAspSerAlaVal 20
 Db 688 ATGATGATGACCACTGACGAGAGAGATTCGAGTTCAAGAGCTTCTCTATTTC 747
 Qy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnLeuGluValAlaLeuValThr 40
 Db 748 GACAAGATGGGAGCGGACCATCCACCAAGAGACTTGGACCGCTTATGAGTCCCT 807
 Qy 41 GlyIleAsnLeuSerGluAlaGlnLeuArgIleSerGluValAspSerAspGly 60
 Db 808 GGCACAAACCAACGAGAGAGATTCGAGATTCATGAACTGATGCTGATGCG 867
 Qy 61 AspGlyLeuIleSerPheGlnGluPheLeuThr--AlaIleArgIleValArg 77
 Db 868 AATGGAAAGATTTACTTCTGATTTCTTACTGATGCTGAGAAATGAGAGACACA 927
 Qy 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgIleAspGlyAspGlyHis 97
 Db 928 GACAGCGAAGAGAAATCCGAGATTCGCGTGTTCACAAGATGGGAGCGCTAC 987
 Qy 98 IleThrValAspGluLeuArgIleValAlaPheArgIleGluGlnProLeuProGlnGlu 117
 Db 988 ATCAGCGCTCTGATTTACTGATGCTGATGCAAAACCTCGGAGAGATTAAACAGATGAA 1047
 Qy 118 GluLeuAspAlaMetIleArgIleValAlaAspValAspGlnAspGlyValAspGly 137
 Db 1048 GAAGTTGATCAATATGATGAGAGAGAGATTCGATGCTGATGCGCAAGTAATATGAA 1107
 Qy 138 GluPheAlaArgMetLeu 143
 Db 1108 GAGTTGTACAAATGATG 1125

RESULT 6
 US-08-818-253-5
 ; Sequence 5, Application US/08818253
 ; Patent No. 5998204
 ; GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.
 APPLICANT: Miyawaki, Atsushi
 TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
 TITLE OF INVENTION: DETECTION OF ANALYTES
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/818, 253
 FILING DATE: 14-MAR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Hallie, Ph.D., Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07257/043001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1929 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 1...1926
 US-08-818-253-5

Alignment Scores:
 Pred. No.: 4.65e-37 Length: 1929
 Score: 373.50 Matches: 74
 Percent Similarity: 73.29% Conservative: 33
 Best Local Similarity: 50.68% Mismatches: 36
 Query Match: 51.23% Indels: 3
 Gaps: 2

US-10-031-403-1 (1-146) x US-08-818-253-5 (1-1929)

Qy 1 MetAlaGlyLeuThrProGluGluAlaGlnTyrIleuValAspSerAlaVal 20
 Db 688 ATGATGATGACCACTGACGAGAGATTCGAGTTCAAGAGAGCTTCTCTATTTC 747
 Qy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnLeuGluValAlaLeuValThr 40
 Db 748 GACAAGATGGGAGCGGACCATCCACCAAGAGACTTGGACCGCTTATGAGTCCCT 807
 Qy 41 GlyIleAsnLeuSerGluAlaGlnLeuArgIleSerGluValAspSerAspGly 60
 Db 808 GGCACAAACCAACGAGAGAGATTCGAGATTCATGAACTGATGCTGATGCG 867
 Qy 61 AspGlyLeuIleSerPheGlnGluPheLeuThr--AlaIleArgIleValArg 77
 Db 868 AATGGAAAGATTTACTTCTGATTTCTTACTGATGCTGAGAAATGAGAGACACA 927
 Qy 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgIleAspGlyAspGlyHis 97
 Db 928 GACAGCGAAGAGAAATCCGAGATTCGCGTGTTCACAAGATGGGAGCGCTAC 987
 Qy 98 IleThrValAspGluLeuArgIleValAlaPheArgIleGluGlnProLeuProGlnGlu 117


```

Db 988 ATCAGCCGCTGCTACGTACCTGACAGCAACCTCGGGAGAGATTACAGATGAA 1047
Oy 118 GluLeuAspAlaMetIleArgGluAlaAspValaAspGlyArgValaAsnTyrGlu 137
Db 1048 GAAGTTGTAAGAAATGATAAGGAGACAGATATGATGTGATGCCAAGTAACATATGAA 1107
Oy 138 GlupheAlaArgMetLeu 143
Db 1108 GAGTTTGTACAATATGATG 1125

RESULT 7
US-08-818-252-5
; Sequence 5, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/818,252B
; CURRENT FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1929
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (0)...(1926)
US-08-818-252-5

Alignment Scores:
Pred. No.: 4,65e-37 Length: 1929
Score: 373.50 Matches: 74
Percent Similarity: 73.29% Conservative: 33
Best Local Similarity: 50.68% Mismatches: 36
Query Match: 51.23% Indels: 3
DB: 4 Gaps: 2

US-10-031-403-1 (1-146) x US-08-818-252-5 (1-1929)
Oy 1 MetalaglyGluLeuThrProGluGluAlaGlnTyrLysAlaIleAspSerAlaVal 20
Db 688 ATGCATGACCACTGACAGACAGATGCGAGATTCAAGAGACCTTTCATTTATTC 747
Oy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
Db 748 GACAGAGATGGGGAGCGGCACCATCACCAAGGAAGAACTTGCGATTGAGGTGCGCT 807
Oy 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValaIleAspSerAspGly 60
Db 808 GGACAAACCCCAACGAGACAGAAATTCAGATATGATCAAGAGTCATCTGATGCGC 867
Oy 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
Db 868 ATGAGACGATTACTTCTTCGTAATTTCTTACTATGATGGCTAGAAATAATGAGGACACA 927
Oy 78 AlaGlyLeuGluAspLeuGlnValaAlaPheArgAlaPheAspGluAspGlyAsnLys 97
Db 928 GACACGAGAAAGAGAAATCGAGACATTCGCTGTTTTCACAAAGATGGGAAGCGCTAC 987
Oy 98 IleThrValaAspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuDuProGlnGlu 117
Db 988 ATCAGCCGCTGCTACGTACGTCACGTCACAAACCTCGGGAGAGATTAAACAGATGAA 1047
Oy 118 GluLeuAspAlaMetIleArgGluAlaAspValaAspGlyArgValaAsnTyrGlu 137
Db 1048 GAAGTTGTAAGAAATGATAAGGAGACAGATATGATGTGATGCCAAGTAACATATGAA 1107
Oy 138 GlupheAlaArgMetLeu 143

```

```

Db 1108 GAGTTTGTACAATATGATG 1125

RESULT 8
US-08-818-253-7
; Sequence 7, Application US/08818253
; Patent No. 5998204
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,253
; FILING DATE: 14-MAR-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1971 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1968
US-08-818-253-7

Alignment Scores:
Pred. No.: 4,79e-37 Length: 1971
Score: 373.50 Matches: 74
Percent Similarity: 73.29% Conservative: 33
Best Local Similarity: 50.68% Mismatches: 36
Query Match: 51.23% Indels: 3
DB: 2 Gaps: 2

US-10-031-403-1 (1-146) x US-08-818-253-7 (1-1971)
Oy 1 MetalaglyGluLeuThrProGluGluAlaGlnTyrLysAlaIleAspSerAlaVal 20
Db 736 ATGCATGACCACTGACAGACAGATGCGAGATTCAAGAGACCTTTCATTTATTC 795
Oy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
Db 796 GACAGAGATGGGGAGCGGCACCATCACCAAGGAAGAACTTGCGATTGAGGTGCGCT 855
Oy 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValaIleAspSerAspGly 60
Db 856 GGACAAACCCCAACGAGACAGAAATTCAGATATGATCAAGAGTCATCTGATGCGC 915
Oy 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77

```

Db 916 AATGGAAGATTTACTTCTTCTGAAATTTCTTACTTGATGGCTAGAGAAAATAGAGACACA 975
Qy 78 AlaglyleugluaspLeuglnValAlapheargAlapheaspGlnaspGlyAspGlyHis 97
Db 976 GACAGCGAGAGGAAATCCGAGAGCATTCGGTGTGTTTGACAGAGATGGAGAGGGCTAC 1035
Qy 98 IllethValaspGluLeuArgArgAlaMetAlaGlyleuglnProLeuProGlnGlu 117
Db 1036 ATCAGCGCTGCTCAGTTACGTCACGTCACAAACCTCGGGGAGAGTTAACAGATGAA 1095
Qy 118 GluLeuaspAlaMetIleArgGluAlaaspValaspGlnaspGlyArgValaspGlyHis 137
Db 1096 GAAGTTGATGAATGATGAAGGAAAGGAGATATCATGTGTATGGCCAAGTAACTATGAA 1155
Qy 138 GluphealAargMetLeu 143
Db 1156 GAGTTTGTACAAATGATG 1173

RESULT 9

US-08-818-252-7
; Sequence 7, Application US/08018252B
; Patent No. 6197928
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/818,252B
; CURRENT FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 1971
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (0)...(1968)
US-08-818-252-7

Alignment Scores:
Pred. No.: 4,79e-37 Length: 1971
Score: 373.50 Matches: 74
Percent Similarity: 73.298 Conservative: 33
Best Local Similarity: 50.688 Mismatches: 36
Query Match: 51.238 Indels: 3
DB: 4 Gaps: 2

US-10-031-403-1 (1-146) x US-08-818-252-7 (1-1971)

Qy 1 MetAlaGlyLeuLeuThrProGlnGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
Db 736 ATGATGATGACCACTGACAGAGAGATGTCAGAGTTCAAGAGCCTTCTCATTTATTC 795
Qy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGluAlaAlaLeuLysAlaThr 40
Db 796 GACAAGATGGGAGCGCACCATCATCACCAAGAGAACTTGGACCGTTATGAGGTGCTT 855
Qy 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValaAspSerAspGly 60
Db 856 GGACAAACCAACCAAGAGAGAGATGCAAGATATGATCATGATGATGATGATGATGATG 915
Qy 61 AspGlyGluIleSerPheGlnGluPheLeuThr--AlaAlaArgLysAlaArg----- 77
Db 916 AATGAGACGATTTACTTCTTCTGAAATTTCTTATCATGATGCGTAAAGAAATGAGAGACA 975
Qy 78 AlaglyleugluaspLeuglnValAlapheargAlaPheaspGlnaspGlyArgGlyHis 97
Db 976 GACAGCGAGAGAGAAATCCGAGAGCATTCGGTGTGTTTGACAGAGATGGAGAGGGCTAC 1035
Qy 98 IllethValaspGluLeuArgArgAlaMetAlaGlyleuglnProLeuProGlnGlu 117

Db 1036 ATCAGCGCTGCTCAGTTACGTCACGTCATGACAAACCTCGGGGAGAGTTAACAGATGAA 1095
Qy 118 GluLeuaspAlaMetIleArgGluAlaaspValaspGlnaspGlyArgValaspGlyHis 137
Db 1096 GAAGTTGATGAATGATGAAGGAAAGGAGATATCATGTGTATGGCCAAGTAACTATGAA 1155
Qy 138 GluphealAargMetLeu 143
Db 1156 GAGTTTGTACAAATGATG 1173

RESULT 10

US-08-100-874-1
; Sequence 1, Application US/08100874
; Patent No. 5498533
; GENERAL INFORMATION:
; APPLICANT: Pooviah, B. W.
; APPLICANT: Takezawa, D.
; APPLICANT: Han, T. J.
; APPLICANT: An, G. H.
; TITLE OF INVENTION: Control of Growth and Development of
; TITLE OF INVENTION: Potato Plants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,874
; FILING DATE: July 30, 1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REFERENCE/DOCKET NUMBER: 7555-00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 641-1600
; TELEFAX: (313) 641-0270
; TELEX: 287637 Harness UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 906 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Solanum tuberosum
; INDIVIDUAL ISOLATE: P-PCM-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 81..530
US-08-100-874-1

Alignment Scores:
Pred. No.: 2.84e-35 Length: 906
Score: 355.50 Matches: 73
Percent Similarity: 69.868 Conservative: 29
Best Local Similarity: 50.008 Mismatches: 41
Query Match: 48.778 Indels: 3
DB: 1 Gaps: 2

US-10-031-403-1 (1-146) x US-08-100-874-1 (1-906)

Qy 1 MetAlaGlyLeuLeuThrProGlnGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20

```

||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db 81 ATGGCAGACGACCTGACGAGAGAGACGATGCCGAGTTCAAGAGACTTTAGCCTTTTC 140
Qy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 141 GCAAGAGATGGCGATGGCTGTATTAATACCAAGAGAGATGGGAACAGTGTATGATCTT 200
Qy 41 GlyLysAsnLeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValAlaSerAspGly 60
Db 201 GGTCAAGATCCCACTGAACCTGACTACAGATATGATAGTGAAGCTGATCTGATCAG 260
Qy 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
Db 261 AATGCAACCATGATTTCTCCAGAGTTCTGATCTGATGCGACGTAAGATGAAGACACT 320
Qy 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
Db 321 GATTCTGACGAGCACTCAAGAGCCTTTCAGAGTTTTCGATGAATGAGATGAAGACACT 380
Qy 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
Db 381 ATTCTGCAAGCTGACCTGCTGATGTAATGACAACCTTGAGAGAGAGCTGACTATGAA 440
Qy 118 GluLeuAspAlaMetIleArgGlnAlaAspValAspGlnAspGlyArgValAsnArgLys 137
Db 441 GAGGTGATGATGATGATCCGAGAGCAGATATTGATGATGGCAGACTAATTATGTAG 500
Qy 138 GluPheAlaArgMetLeu 143
Db 501 GAGTTTGTCCGTATGATG 518

RESULT 11
US-09-239-909-1
; Sequence 1, Application US/09239909
; Patent No. 6284952
; GENERAL INFORMATION:
; APPLICANT: Kumo Petrochemical Co. Ltd.
; TITLE OF INVENTION: Transgenic Plants with Divergent SCAM4 or SCAM5 Gene to Achieve
; FILE REFERENCE: P99-2-6
; CURRENT APPLICATION NUMBER: US/09/239,909
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: EP 99300136.1
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 1
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: G. max calmodulin4 (SCAM4)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (657)..(1106)
US-09-239-909-1

Alignment Scores:
Pred. No.: 3,64e-31 Length: 1401
Score: 324.50 Matches: 65
Percent Similarity: 67.81% Conservative: 34
Best Local Similarity: 44.52% Mismatches: 44
Query Match: 44.51% Indels: 3
DB: 4 Gaps: 2

US-10-031-403-1 (1-146) x US-09-239-909-1 (1-1401)
Qy 1 MetAlaGlyGluLeuThrProGlnGluGlnAlaGlnIleTyLysLysAlaPheSerAlaVal 20
Db 657 ATGCGAGATATCTCTGAGTGAAGACAGATGTTGATTTTAAAGAGCCTTGGCTTGT 716
Qy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 717 GACAAAGATGAGATGCTTACTGTGGAAGAACTGCCACAGTCTATTCGGTCATTC 776
Qy 41 GlyLysAsnLeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValAlaSerAspGly 60

```

```

..... ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db 777 GATCAAGAACCCCACTGAAGAGAGCTCAAGATATGATTAAGCAAGTTCATGAGATGGC 836
Qy 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 837 AATGCAACCATGAATTAACGAGTTCCTGACCTTGATGCGCCAAAGAACTTAAGACACT 896
Qy 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
Db 897 GATGCAAGAGAGAGCTCAAGAGACTTTTCAGAGTTTTCGACAAAGATCAAAATGCTAC 956
Qy 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
Db 957 AATACAGAGTGAAGTGTGACACCACTAATGATCAATCTAAGGGGAAAAGTAAACCATGAA 1016
Qy 118 GluLeuAspAlaMetIleArgGlnAlaAspValAspGlnAspGlyArgValAsnArgLys 137
Db 1017 GAGGTGACAGATGATTTAAAGACAGATTTGACGATGATGCCCAAGTAACTATGAG 1076
Qy 138 GluPheAlaArgMetLeu 143
Db 1077 GAATTCGTCAAGTATGATG 1094

RESULT 12
US-09-239-909-3
; Sequence 3, Application US/09239909
; Patent No. 6284952
; GENERAL INFORMATION:
; APPLICANT: Kumo Petrochemical Co. Ltd.
; TITLE OF INVENTION: Transgenic Plants with Divergent SCAM4 or SCAM5 Gene to Achieve
; FILE REFERENCE: P99-2-6
; CURRENT APPLICATION NUMBER: US/09/239,909
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: EP 99300136.1
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 3
; LENGTH: 916
; TYPE: DNA
; ORGANISM: G. max calmodulin5 (SCAM5)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)..(518)
US-09-239-909-3

Alignment Scores:
Pred. No.: 4,64e-29 Length: 916
Score: 305.50 Matches: 62
Percent Similarity: 63.70% Conservative: 31
Best Local Similarity: 42.47% Mismatches: 50
Query Match: 41.91% Indels: 3
DB: 4 Gaps: 1

US-10-031-403-1 (1-146) x US-09-239-909-3 (1-916)
Qy 1 MetAlaGlyGluLeuThrProGlnGluGlnAlaGlnIleTyLysLysAlaPheSerAlaVal 20
Db 69 ATGCGAGATGTTCTGATGAAGACAGATTAATGATCAAAAGAACCTTGGCTTGT 128
Qy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 129 GACAAAGATGATGATGGTCAATTAATGACGAAATTTGTCACGGTTATCCGGTCATG 188
Qy 41 GlyLysAsnLeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValAlaSerAspGly 60
Db 189 GTTCAGAACCCCACTGAAGAGAGCTCCCAAGATGATTAAGAGAGGTATGATCCAGATG 248
Qy 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 249 AATGCAACCATGATTTCTGATTTTGAACCTTAATGCGCCAAAGAAATGAAGAACT 308
Qy 81 -----GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97

```

Db 309 GATCAGAGGAGATCTCAAGAGCTTTCAGGTGTTGACAGGATCAAAATGGCTAC 368
Qy 98 ILeThraVlaSpLeuArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
Db 369 ATTTCAGCAATGAGTGTGAGACAGTATATCATCATCTGGGTGAAAACCTAACGATGAG 428
Qy 118 GlueuAspAlaMetIleArgGlnAlaAspValAspGlnArgValAsnTyGlu 137
Db 429 GAGGTGGACGATGATGAAGAAGCATTTGATGCTGATGCTCAAGTTAATATGAT 488
Qy 138 GluPheAlaArgMetLeu 143
Db 489 GAATTGTCAGATGATG 506
RESULT 13
US-09-285-601-1
Sequence 1, Application US/09285601
Patent No. 6248528
GENERAL INFORMATION:
APPLICANT: Chen, Hong
APPLICANT: Frelmer, Nelson
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
FILE REFERENCE: 7853-089
CURRENT APPLICATION NUMBER: US/09/285, 601
EARLIER FILING DATE: 1999-04-02
EARLIER APPLICATION NUMBER: 60/080, 841
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 1
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (49)..(564)
US-09-285-601-1
Alignment Scores:
Pred. No.: 1,49e-26 Length: 1173
Score: 286.50 Matches: 62
Percent Similarity: 62.24% Conservative: 27
Best Local Similarity: 43.36% Mismatches: 51
Query Match: 39.30% Indels: 3
Gaps: 1
US-10-031-403-1 (1-146) x US-09-285-601-1 (1-1173)
Qy 4 GlueuThrProGlnGluGlnAlaGlnTyrlsAlaPheSerAlaValAspThrAsp 23
Db 118 GAGCTCACTGAGATCGAAGCAAGATTCGGGACATTTGACCTTCGACGTGAC 177
Qy 24 GlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThrGlyLysAsn 43
Db 178 GGAAGTGGACCATCGACGGGAAGACCTGAGGTGCCATGAGAGCGCTGGCTTGAA 237
Qy 44 LeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValAspSerAspGlyAspGlu 63
Db 238 CCCAGGAGAGAGATGAGAAATGATCTCCAGGTGACAGGAGGAGGAGGAGAG 297
Qy 64 IleSerPheGlnGluPheLeu-----ThAlaAlaArgLysAlaArgAlaGlyLeu 80
Db 298 ATGAGCTTCATGACTCTGGCGGTGATGACGAGAGATGTCGAGAGGACACCAA 357
Qy 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAsnIleThrVal 100
Db 358 GAAGAAATCTGGAAGGCTTCAGGCTTTGATGACATGAGACCGGGAAGATCTGCTC 417
Qy 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlnGlu 120
Db 418 AAAAAGCTGAAGCGTGTGGCCAGACGACCTGGGGAGAACTCAAGGATGAGAGCTGAC 477

Qy 121 AlaMetIleArgGlnAlaAspValAspGlnAspGlyArgValAsnTyGlnGluPheAla 140
Db 478 GAGATGATCGACGAGAGCTGATCGGATGGGACCGGAGAGTGAACGAGAGATTCCT 537
Qy 141 ArgMetLeu 143
Db 538 CGGATCATG 546
RESULT 14
US-09-285-601-3
Sequence 3, Application US/09285601
Patent No. 6248528
GENERAL INFORMATION:
APPLICANT: Chen, Hong
APPLICANT: Frelmer, Nelson
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
FILE REFERENCE: 7853-089
CURRENT APPLICATION NUMBER: US/09/285, 601
EARLIER FILING DATE: 1999-04-02
EARLIER APPLICATION NUMBER: 60/080, 841
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
LENGTH: 6709
TYPE: DNA
ORGANISM: Homo sapiens
US-09-285-601-3
Alignment Scores:
Pred. No.: 1,62e-25 Length: 6709
Score: 286.50 Matches: 62
Percent Similarity: 62.24% Conservative: 27
Best Local Similarity: 43.36% Mismatches: 51
Query Match: 39.30% Indels: 3
Gaps: 1
US-10-031-403-1 (1-146) x US-09-285-601-3 (1-6709)
Qy 4 GlueuThrProGlnGluGlnAlaGlnTyrlsAlaPheSerAlaValAspThrAsp 23
Db 3015 GAGCTCACTGAGATCGAAGCAAGATTCGGGACATTTGACCTTCGACGTGAC 3074
Qy 24 GlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThrGlyLysAsn 43
Db 3075 GGAAGTGGACCATCGACGGGAAGACCTGAGGTGCCATGAGAGCGCTGGCTTGA 3134
Qy 44 LeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValAspSerAspGlyAspGlu 63
Db 3135 CCCAGGAGAGAGATGAGAAATGATCTCCAGGTGACAGGAGGAGGAGGAGGAG 3194
Qy 64 IleSerPheGlnGluPheLeu-----ThAlaAlaArgLysAlaArgAlaGlyLeu 80
Db 3195 ATGACTTCATGACTCTCTGCGGTGATGACGAGAGATGTCGAGAGGAGACCAA 3254
Qy 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAsnIleThrVal 100
Db 3255 GAAGAAATCTGGAAGGCTTCAGGCTTTGATGACATGAGACCGGGAAGATCTGCTC 3314
Qy 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlnGlu 120
Db 3315 AAAAAGCTGAAGCGTGTGGCCAGACGACCTGGGGAGAACTCAAGGATGAGAGCTGAC 3374
Qy 121 AlaMetIleArgGlnAlaAspValAspGlnAspGlyArgValAsnTyGlnGluPheAla 140
Db 3375 GAGATGATCGACGAGCTGATCGGATGGGACGCGAAGTGAACGAGAGATTCCTT 3434
Qy 141 ArgMetLeu 143
Db 3435 CGGATCATG 3443

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 16, 2003, 03:19:19 ; Search time 1748 Seconds
(without alignments)
1352.712 Million cell updates/sec

Title: US-10-031-403-1
Perfect score: 729
Sequence: 1 MAGELPDEEAQYKAFSAV.....DVDQGRVNEEFARMLAE 146

Scoring table: BIOSUM62
Xgapop 10.0, Ygapext 0.5
Ygapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 segs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV-rlh
-MODEL-frame+ p2n model -DEV-rlh
-O=/cgnr/_1/USPRO.spool/US10031403/runat_08052003.131925.5691/app.query.fasta_1.327
-DB-EST -QFMT-fastlap -SUFF1-rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX-biosum62 -TRANS-human40.cdi -LIST=45
-DOCLLIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10031403.ecgn.1.1.1906.runat.08052003.131925.5691 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOC -DEV-TIMEOUT=120
-WAIT_TIMEOUT=30 -THRAIDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estlov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	726	99.6	721	12	BG696865
2	725	99.5	819	12	BG680086
3	725	99.5	867	12	BG697492
4	703	96.4	830	12	BG743203
5	699	95.9	976	12	BG676307
6	642	88.1	508	9	AT191325
7	642	88.1	508	9	AT191495
8	411	56.4	444	10	AM464722
9	398.5	54.7	537	10	BE012482
10	391.5	53.7	846	12	BF103910
11	390.5	53.6	499	9	AA770786
12	390.5	53.6	619	10	BE199943
13	389.5	53.4	603	12	BF297037
14	389.5	53.4	619	12	BF297132
15	389.5	53.4	746	13	BM160783
16	389.5	53.4	765	13	BM171356
17	389.5	53.4	781	13	BM164242
18	388.5	53.3	510	9	AA023153
19	388.5	53.3	517	13	BI936031
20	388.5	53.3	554	14	BM874967
21	388.5	53.3	596	10	AM765916
22	388.5	53.3	613	14	BO633415
23	388.5	53.3	659	14	BM837142
24	388.5	53.3	908	9	AU079535
25	388.5	53.3	939	13	BM542199
26	387.5	53.2	646	13	BG974147
27	386.5	53.0	521	14	W10714
28	386.5	53.0	524	12	BE737663
29	386.5	53.0	573	14	BM839707
30	386.5	53.0	669	12	BG547553
31	386.5	53.0	718	12	BG705382
32	386.5	53.0	719	12	BG777110
33	386.5	53.0	755	12	BG699270
34	386.5	53.0	814	13	BI668543
35	386.5	53.0	816	12	BF666722
36	386.5	53.0	859	12	BG723224
37	386.5	53.0	869	12	BG703957
38	386.5	53.0	878	12	BE666960
39	386.5	53.0	883	12	BE696541
40	386.5	53.0	914	12	BG542960
41	385.5	52.9	565	10	AM537180
42	385.5	52.9	574	13	BI865062
43	385.5	52.9	620	12	BG507134
44	385.5	52.9	637	12	BG776331
45	385.5	52.9	712	10	AV715763

ALIGNMENTS

RESULT 1
LOCUS BG696865 721 bp mRNA EST 07-MAY-2001
DEFINITION 602658626f1 NCI_CGAP_Skn3 Homo sapiens CDNA clone IMAGE:4801854 5',
RNA sequence.
ACCESSION BG696865
VERSION BG696865.1 GI:13962457
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 721)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10695 row: c column: 07
High quality sequence stop: 697.

FEATURES
source
1. 721
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4801854"
/clone_lib="NCI CGAP_Skn3"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Skin; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 125 a 221 c 271 g 104 t

ORIGIN

Alignment Scores:
Pred. No.: 5,66e-78 Length: 721
Score: 726.00 Matches: 145
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.32% Mismatches: 0
Query Match: 99.59% Indels: 0
Gaps: 0

US-10-031-403-1 (1-146) x BG696865 (1-721)

QY 1 MetAlAGlGluLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
Db 100 ATGGCCGAGTGAAGTCTCTGAGAGAGAGCCAGTACAAAGGCTTCTCCGCGGT 159

QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuAlaAlaLeuLysAlaThr 40
Db 160 GACACGATGGAAGGACACATCAATGCCAGAGCTGGCGCGCGCTGAAGGCCACG 219

QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
Db 220 GGCAGAACCTCTCGAGGCCCGCAAGAACTCATCTCCGAGGTTGACAGCGCGC 279

QY 61 AspGluGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaAlaGlyLeu 80
Db 280 GACGCGCAAAATCAAGCTTCCAGAGTTCCTACGCGGCGGAAGGCGCGGCGCTG 339

QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyHisIleThrVal 100
Db 340 GAGGACCTGAGGTGCGCTTCCGCGCTTGCACAGATGGCGACGCCCATCACCGTG 399

QY 101 AspGluLeuArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluGluLeuAsp 120
Db 400 GACGAGCTCAAGCGGCGCAAGCGGCGCTGGCGCAGCCGCTCCGACGAGAGCTGGAC 459

QY 121 AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGluGluPheAla 140
Db 460 GCCATGATCCGCGAGCGCGAGCTGACACAGAGCGGCGGTGAACATGAGAGTTGCGC 519

QY 141 ArgMetLeuAlaGlnGlu 146
Db 520 AGGATGCTGCCCGACGAG 537

RESULT 2
LOCUS BG680086 819 bp mRNA linear EST 01-MAY-2001
DEFINITION 60268238F1 NCI CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4753280 5',
mRNA sequence.

ACCESSION BG680086
VERSION BG680086.1 GI:13911483
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 819)
AUTHORS NIH-MGC <http://imgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10612 row: k column: 09
High quality sequence stop: 819.

FEATURES
source
1. 819
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4753280"
/clone_lib="NCI CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Skin; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 139 a 256 c 300 g 124 t

ORIGIN

Alignment Scores:
Pred. No.: 9e-78 Length: 819
Score: 725.00 Matches: 145
Percent Similarity: 99.32% Conservative: 0
Best Local Similarity: 99.32% Mismatches: 1
Query Match: 99.45% Indels: 0
Gaps: 0

US-10-031-403-1 (1-146) x BG680086 (1-819)

QY 1 MetAlAGlGluLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
Db 117 ATGGCCGAGTGAAGTCTCTGAGAGAGAGCCAGTACAAAGGCTTCTCCGCGGT 176

QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuAlaAlaLeuLysAlaThr 40
Db 177 GACACGATGGAAGGACACATCAATGCCAGAGCTGGCGCGCGCTGAAGGCCACG 236

QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
Db 177 GACACGATGGAAGGACACATCAATGCCAGAGCTGGCGCGCGCTGAAGGCCACG 236

QY 61 AspGluGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaAlaGlyLeu 80
Db 237 GGCAGAACCTCTCGAGGCCCGCAAGAACTCATCTCCGAGGTTGACGCGGACGCGC 296

QY 101 AspGluLeuArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluGluLeuAsp 120
Db 297 GACGCGCAAAATCAAGCTTCCAGAGTTCCTACGCGGCGGAAGGCGCGGCGCTG 356

QY 141 ArgMetLeuAlaGlnGlu 146
Db 357 GAGGACCTGAGGTGCGCTTCCGCGCTTGCACAGATGGCGACGCCCATCACCGTG 416

QY 101 AspGluLeuArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluGluLeuAsp 120
Db 417 GACGAGCTCAAGCGGCGCAAGCGGCGCTGGCGCAGCCGCTCCGACGAGAGCTGGAC 476

QY 121 AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGluGluPheAla 140
Db 121 AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGluGluPheAla 140

Qy 1 MetalaglycylleuthrProglnglgluinalglntrylsylsalapheserAlaVal 20
Db 78 ATGGCGGGTGAACGTACCTCCGAGAGAGAGGCCCAAGTACAAAAGCGTTTCTCCGCGTT 133
Qy 21 AspThrAspGlyAsnGlyThrTleAsnAlaGlnGluLeuGlyAlaAlaLeuYsAlaThr 40
Db 138 GACACGGATGGAAGAACGGCACCATCAATGCCAGAGAGCTGGGGCGGGCGTGAAGGCCACG 197
Qy 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
Db 198 GGCAGAAACCTCTCGGAGGCCCACTAAGAAACTCATCTCCGAGGTGACGGCGACGGC 257
Qy 61 AspGlyLysIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
Db 258 GACGGCGAAATCAGCTTCCAGGAATTCCTGACGGCGGCAAGAAAGGCCAGAGCGCGGCTG 317

Qy 1 MetalalgiyluleuthProcluglualaglnTyrlLysylalapheseralaval 20
 Db 121 ATGGCCGGTGAAGCTCAGTCCTGAGGAGAGGCCCAAGTACAAAAGCCTTCTCCGGGTT 18
 Qy 21 AsprthraspGlyasnGlyThrIleasnalaglngluleu-GlyalalalaleLysalath 40

Db 181 GACACGATGAAAGCACCACATCATGCCAGAGCTGTGCGCGCTGAAGGCCAC 240
 QY 40 rgllytysasnleuSercIuaInleuArglySleuIleSercIuValaAspSeraSpI 60
 Db 241 GGGCAAGAACCTCTCGAGAGCCAGCTAAGAAACTCATCTCCGAGGTTGACGGCGACG 300
 QY 60 yaspIgluIleSerpheInglupheleuthrAlaAlaArglySAlaArgAlaGlyle 80
 Db 301 CGAGCGGGAATCAGCTTCAGAGATTCTCAGCGCGCGCAAGAGGCCAGCGCGCTCT 360
 QY 80 ugiuAspIleuGluValaAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVa 100
 Db 361 GGAGGACCTCAGAGCTGCTTCGCGCTTCGACAGAGATGGCGACCGCATCACCCT 420
 QY 100 laspIuIleuArgAlaMetaIaGlyLeuGlyGlnProIeuProGlnIuGlyleuAs 120
 Db 421 GGACGAGCTCAGCGCGGCGCATGGCGGGGCTGGGGCGACCGCTGCGCGAGAGAGCTGGA 480
 QY 120 palameIleArgGluAlaAspValaAspGlnAspGlyArgValaAsnTyrGluIuPheAl 140
 Db 481 CGCATGATCCGGAGCGCCAGCTGACGAGAGCGGGGTGAACATACAGAGAGATTGCG 540
 QY 140 aArgMetIeuaIaGlnIu 146
 Db 541 GAGATGCTCGCCAGAG 559

RESULT 5
 BG676307 976 bp mRNA linear EST 01-MAY-2001
 LOCUS 602622717F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4747661 5',
 DEFINITION mRNA sequence.
 ACCESSION BG676307
 VERSION BG676307.1 GI:13907703
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 976)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLNL0598 row: a column: 06
 High quality sequence stop: 820.
 Location/Qualifiers
 1. 976

FEATURES
 source
 1. 976

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4747661"
 /clone_1lb="NCI_CGAP_Skn4"
 /tissue_type="squamous cell carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI;
 Site:2: SalI; Cloned unidirectionally.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 234 a 263 c 342 g 137 t

Alignment Scores:
 Pred. No.: 1.66e-74 Length: 976
 Score: 699.00 Matches: 144
 Percent Similarity: 99.32% Conservative: 1
 Best Local Similarity: 98.63% Mismatches: 1

Query Match: 95.88% Indels: 1
 DB: 12 Gaps: 0
 US-10-031-403-1 (1-146) x BG676307 (1-976)

QY 1 MetIaGlyIuLeuThrProGlnIuGluAlaGlnTyrIlySAlaPheSerAlaVal 20
 Db 115 ATGGCCGGTGAAGCTCTCGAGAGAGAGCCAGTACAAAGAGGCTTCTCCGCGTT 174
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnIuLeuGlyAlaAlaLeuValaThr 40
 Db 175 GACACGATGAAAGCACCACATCATGCCAGAGCTGGGCGCGGCTGAAGGCCACG 234
 QY 41 GLyAsnleuSercIuaInleuArglySleuIleSercIuValaAspSeraSpI 60
 Db 235 GGCAGAACCTCTCGAGAGCCAGCTAAGAACTCATCTCCGAGGTTGACAGCGAGCG 294
 QY 61 AspIgluIleSerpheInglupheleuthrAlaAlaArglySAlaArgAlaGlyleu 80
 Db 295 GAGCGGAAATCAGCTTCAGAGATTCTCAGCGCGCGGAAGAGCGCAGGC-GGCTG 353
 QY 81 GluAspIleuGlnValaAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
 Db 354 GAGGACCTCGACGTCGCTTCGCGCTTCGACAGAGATGGCGAGCCACATCACCCTG 413
 QY 101 AspIuIleuArgAlaMetaIaGlyLeuGlyGlnProIeuProGlnIuGlyleuAsp 120
 Db 414 GACGAGCTCAGCGCGGCGCATAGCGGGCTGGCGCGCGCTGCGCGAGAGAGACTGGAC 473
 QY 121 AlameIleArgGluAlaAspValaAspGlnAspGlyArgValaAsnTyrGluIuPheAla 140
 Db 474 GCCATGATCCGGAGCGCGGCGAGCTGACAGAGAGCGGGGTGAACATACAGAGATTGCG 533
 QY 141 ArgMetIeuaIaGlnIu 146
 Db 534 AGATGCTCGCCAGAG 551

RESULT 6
 AT791325 508 bp mRNA linear EST 24-OCT-2000
 LOCUS ae56g09.y5 StrataGene lung carcinoma 937218 Homo sapiens cDNA clone
 DEFINITION IMAGE:950944 5' similar to SW:CALM_PLAFA P24044 CALMODULIN.; mRNA
 sequence.
 ACCESSION AT791325
 VERSION AT791325.1 GI:5339041
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 508)
 AUTHORS NCI-CGAP http://www.nci.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 COMMENT other_ESTS: ae56g09.y5
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 This read is a RESEQUENCE of a previously sequenced human clone
 Original clone citation: see original entry for original citation
 information
 This 5' resequenced clone has no previous 5' data to verify this
 new read against
 Insert Length: 587 Std Error: 0.00
 Seq primer: -40RP from Glibco
 High quality sequence stop: 486.
 Location/Qualifiers
 1. 508

FEATURES
 source
 1. 508

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:950944"

```

/clone_lib="Stratagene lung carcinoma 937218"
/tissue_type="lung carcinoma"
/cell_line="NCI-H69"
/dev_stage="cell line NCI-H69"
/lab_host="SOLR (Kanamycin resistant)"
/notes="Organ: Lung; Vector: pBluescript SK-; Site: 1: EcoRI
; Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo
dt. Small cell carcinoma cell line NCI-H69. Average
insert size: 1.0 kb; Uni-ZAP XR Vector: -5' adaptor
sequence: 5' GATTCCGACAG 3' -3' adaptor sequence: 5'
CTCAGCTTTTCTTTTCTTTTCTTTT 3'"

```

```

BASE COUNT      100 a      153 c      189 g      65 t      1 others
ORIGIN

```

```

Alignment Scores:
Pred. No.:      5,42e-68      Length:      508
Score:          642.00      Matches:      129
Percent Similarity: 98.47%      Conservative: 0
Best Local Similarity: 98.47%      Mismatches: 2
Query Match:    98.07%      Indels:      0
DB:             Gaps:      0

```

```

US-10-031-403-1 (1-146) x A1791495 (1-508)

```

```

QY 1 MetAlaGlyGluLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
DB 115 ATGGCCGGTACGCTCCTCAGAGAGAGGCCCAAGAAAGCTTCTCCCGCGTT 174
QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleLeuysAlaThr 40
DB 175 GACAGCGATGGAAGGACGACATCAATGCCAGAGAGTGGCGCGCTGAAAGCCACG 234
QY 41 GlyLysAsnLeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValAspSerAspGly 60
DB 235 GGCAAGAACCTCTCGAGAGGCCCAAGAAATCATCTCCGAGTTACGCGCACGCGC 294
QY 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
DB 295 GACGCGCAATCAGCTCCTCAGAGAGTCTCGACGCGCGCAAGAAAGGCGCGCGCTG 354
QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
DB 355 GAGGACCTGACAGTCCCTCCGCGCTTCGACAGAGAGGCGCGCACATCACCGCTG 414
QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGluLeuAsp 120
DB 415 GACGAGCTCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 474
QY 121 AlaMetIleArgGluAlaAspValAspGlnAsp 131
DB 475 GCCATGATCCGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 507

```

```

RESULT 7
A1791495      508 bp      mRNA      linear      EST 13-DEC-1999
LOCUS      n101f09.y5 NCI CGAP Br2 Homo sapiens cDNA IMAGE:966761 5'
DEFINITION      similar to SW:CALM_PLAFA P24044 CALMODULIN.; mRNA sequence.
ACCESSION      A1791495
VERSION      A1791495.1 GI:5339211
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

```

REFERENCE      1 (bases 1 to 508)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Other ESTs: n101f09.s1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nlm.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

```

Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLN at:
www.bio.linn.gov/dbp/image/image.html

This read is a RESEQUENCE of a previously sequenced human clone
 Original clone citation: see original entry for original citation
 Information
 This 5' resequenced clone has no previous 5' data to verify this
 new read against
 Insert Length: 936 Std Error: 0.00
 Seq primer: -40RP from Gibco
 High quality sequence stop: 464.
 Location/Qualifiers

FEATURES

source

1..508

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:966761"

/clone_lib="NCI-CGAP_Br2"

/sex="female, pooled"

/tissue_type="breast"

/lab_host="DH10B"

/note="Vector: p773D-Pac (Pharmacia) with a modified
 polylinker: 1st strand cDNA was prepared from pooled bulk
 breast tumor tissue, and was then primed with a Not I -
 oligo(dt) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified p773
 vector. This library is the normalized version of
 NCI CGAP Br1.1. Library was constructed by Bento Soares
 and M. Fatima Bonaldo."

```

BASE COUNT      100 a      154 c      189 g      64 t      1 others
ORIGIN

```

```

Alignment Scores:
Pred. No.:      5,42e-68      Length:      508
Score:          642.00      Matches:      129
Percent Similarity: 98.47%      Conservative: 0
Best Local Similarity: 98.47%      Mismatches: 2
Query Match:    98.07%      Indels:      0
DB:             Gaps:      0

```

```

US-10-031-403-1 (1-146) x A1791495 (1-508)

```

```

QY 1 MetAlaGlyGluLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
DB 115 ATGGCCGGTACGCTCCTCAGAGAGAGGCCCAAGAAAGCTTCTCCCGCGTT 174
QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleLeuysAlaThr 40
DB 175 GACAGCGATGGAAGGACGACATCAATGCCAGAGAGTGGCGCGCTGAAAGCCACG 234
QY 41 GlyLysAsnLeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValAspSerAspGly 60
DB 235 GGCAAGAACCTCTCGAGAGGCCCAAGAAATCATCTCCGAGTTACGCGCACGCGC 294
QY 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
DB 295 GACGCGCAATCAGCTCCTCAGAGAGTCTCGACGCGCGCAAGAAAGGCGCGCGCTG 354
QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
DB 355 GAGGACCTGACAGTCCCTCCGCGCTTCGACAGAGAGGCGCGCACATCACCGCTG 414
QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGluLeuAsp 120
DB 415 GACGAGCTCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 474
QY 121 AlaMetIleArgGluAlaAspValAspGlnAsp 131

```


US-10-031-403-1 (1-146) x BE199943 (1-619)

```

OY 1 MetAlaGlyLeuLeuThrProGluGluAlaGlnTrpLysLysAlaPheSerAlaVal 20
    |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|
DB 515 ATGGCTGATCAGCTACGAGAAAGAGAGATTGCTGAATTCAGAGAGCTTTCCCTATTC 456
OY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
    |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|
DB 455 GATACAGATGGTGACGGCCACATCCACACCAAGAACTGGGACCTCATCGCGTCACTG 396
OY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
    |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|
DB 395 GGTCAAGAACCCCAAGAACGAGCTGCAAGATGATGATCAACAGAGTGTGATGCTGATGCG 336
OY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
    |||||  ||  ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 335 AATGGCACCATTGACTCCAGATGCTTGAATGATGATGCTGAGAAAATGAAAGACACACA 276
OY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
    |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|
DB 275 GATACGAGAAAGAGATCCGACAGCCCTTCCAGATGTTGACAGAGATGGATGGATTAC 216
OY 98 IleThrValAspGluLeuArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 215 ATCAGTGGCGGACAACTGCGCCACGTCATGACAAACTTAGAGAAAAGCTTACACAGATGAA 156
OY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyValArgValAsnTrpGlu 137
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 155 GAAGTAGATGAATATGATGACAGAGCATGATGATGCGGACGACAACTAATGTGAA 96
OY 138 GluPheAlaArgMetLeu 143
    |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|
DB 95 GAATTCGTACAGATGATG 78

RESULT 13
BF297037 603 bp mRNA linear EST 04-MAY-2001
LOCUS 046bDc10 Pb cDNA #17, Tommaso Pace, Marta Ponzi, and Clara Frontali
DEFINITION Plasmodium berghei cDNA 5', mRNA sequence.
ACCESSION BF297037
VERSION BF297037.1 GI:13948646
KEYWORDS EST.
SOURCE Plasmodium berghei.
ORGANISM Plasmodium berghei.
REFERENCE 1 (bases 1 to 603)
AUTHORS Carlton,J.M.-R. and Dame,J.B.
TITLE The Plasmodium vivax and P. berghei gene sequence tag projects
JOURNAL Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
COMMENT Contact: Dame JB
Department of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611-0880, USA
Tel: 352 392 4700
Fax: 352 392 9704
Email: damej@mail.ufl.edu
Seq primer: f3.

```

FEATURES

Source Location/Qualifiers

1..603

/organism="Plasmodium berghei"

/strain="ANKA clone HP (gametocyte producer)"

/db_xref="taxon:5821"

/clone_lib="Pb cDNA #17, Tommaso Pace, Marta Ponzi, and Clara Frontali"

/dev_stage="asynchronous blood stage"

/lab_host="Wistar rats"

/note="Vector: pBluescript II vector DNA, excised from Lambda Zap II.; Site.1: EcoRI; Site.2: XhoI; Total RNA was extracted from asynchronous blood stage forms of the cloned ANKA isolate of P. berghei, grown in Wistar rats to 30% parasitemia and 2-5% gametocytemia. Contaminating host white cells had previously been removed and final host

cell contamination estimated to be approximately 5%.

PolyA+ RNA was extracted and reverse transcribed using an oligo dT-XhoI primer (lambda Zap II cDNA cloning kit, Stratagene). Second strand cDNA was made following the manufacturer's protocol. EcoRI adaptors were ligated to the cDNA, and fragments were ligated into EcoRI/XhoI digested vector."

BASE COUNT 246 a 68 c 115 g 173 t 1 others

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
318e-37	389.50	603	76
Percent Similarity:	73.97%	Conservative:	32
Best Local Similarity:	52.05%	Mismatches:	35
Query Match:	53.43%	Indels:	3
DB:	12	Gaps:	2

US-10-031-403-1 (1-146) x BF297037 (1-603)

```

OY 1 MetAlaGlyLeuLeuThrProGluGluAlaGlnTrpLysLysAlaPheSerAlaVal 20
    |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|
DB 49 ATGGCAGACAGATTACACAGACAAATTTCTGAATTCAGAGAGCTTTCACTTGT 108
OY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
    |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|
DB 109 GATTAAGATGGAGATGGAACCACTTAACCAAGAAAGAACTGATGCTGATGCTTG 168
OY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
    |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|
DB 169 GGACAAACCCCAAGAACGAGAACTGACAAAGATGATGAATTAAGAAATTCACACAGATGG 228
OY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
    |||||  ||  ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 229 AATGATCAATGATTTCCACAGATTTTAACTTATGCAAGAAATGAAAGATACA 288
OY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
    |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|
DB 289 GATACGAGAAAGATTAATGACATTTAGATTTGATGAGGATGCTGATGATAT 348
OY 98 IleThrValAspGluLeuArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 349 ATCAGTGGCGGACAACTGCGCCACGTCATGACAAACTTAGAGAAAAGCTTACACAGATGAA 408
OY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyValArgValAsnTrpGlu 137
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 409 GAAGTGAATGAATGATTAAGAGAGAACTGACATGATGAGATGACAAATTAATTATGAG 468
OY 138 GluPheAlaArgMetLeu 143
    |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|  |||||  ::::|
DB 469 GAGTTGTTAAATGATG 486

RESULT 14
BF297132 619 bp mRNA linear EST 04-MAY-2001
LOCUS 047bF01 Pb cDNA #17, Tommaso Pace, Marta Ponzi, and Clara Frontali
DEFINITION Plasmodium berghei cDNA 5', mRNA sequence.
ACCESSION BF297132
VERSION BF297132.1 GI:13948827
KEYWORDS EST.
SOURCE Plasmodium berghei.
ORGANISM Plasmodium berghei.
REFERENCE 1 (bases 1 to 619)
AUTHORS Carlton,J.M.-R. and Dame,J.B.
TITLE The Plasmodium vivax and P. berghei gene sequence tag projects
JOURNAL Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
COMMENT Contact: Dame JB
Department of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611-0880, USA
Tel: 352 392 4700
Fax: 352 392 9704

```

Db 245 GGACAAAACCCACCGAGAGACTATGTATTAATTAATTGACACAGATGGA 304

Db 245 GGACAAAACCCACCGAGAGACTATGTATTAATTAATTGACACAGATGGA 304


```

QY 61 AspglygluileserPhecingluPheleuthr---AlaIarglysAlarg----- 77
Db 305 AATGATCAATTGATTTCAGATTTTAACTTAATGCAAGAAAATGAAGATACA 364
QY 78 AlaGlyleugluAspleugluValAlaPheargAlaPheAspgluAspglyHis 97
Db 365 GATACAGAAGAATTAATGAGCATTTAGAGTGTGATGAGATGATGATGATAT 424
QY 98 IleThrValAspgluileuArgArgAlaMetAlaGlyleugluProleuProGlu 117
Db 425 ATCAGTGTGATGAATTAAGACACGTTATGACAACTTAGGGGAAAACCTTACAAATGAA 484
QY 118 GluleuAspAlaMetIleArgGluAlaAspValAspGluAspGlyArgValAsnTYrGlu 137
Db 485 GAAGTGTGATGAATGATAGAGAGAGCTGATATGATGAGATGACAAATTAATTATGAG 544
QY 138 GluPheAlaArgMetLeu 143
Db 545 GAGTTGTAAATGATG 562

```

Search completed: May 16, 2003, 04:58:50
 Job time : 1769 secs

XX DR WPI; 2002-241625/29.
 XX PT Predicting toxic effects of compounds or the progression of these toxic
 PT effects by determining the changes in gene expression in tissues or
 PT cells exposed to the toxin and comparing these to gene expression in
 PT unexposed tissues or cells
 PS Claim 1; Seq ID No 1352; 239pp; English.
 XX
 CC The invention relates to methods for predicting toxic effects of
 CC compounds or the progression of these toxic effects by determining the
 CC global changes in gene expression in tissues or cells exposed to the
 CC toxin and comparing these to gene expression in unexposed tissues or
 CC cells. Also included are methods of predicting at least one toxic
 CC effect of a compound or progression of a toxic effect, preferably the
 CC hepatotoxicity of a compound, comprising detecting the level of
 CC expression in a tissue or cell sample exposed to the compound of two or
 CC more genes listed in the specification, where differential expression of
 CC the genes is indicative of at least one toxic effect or progression.
 CC The method can also be used to identify an agent which modulates the
 CC toxic response and predict cellular pathways that a compound modulates
 CC in a cell. The method utilises a set of at least two probes (on a solid
 CC support in kit form), where each of the probes comprises a sequence that
 CC specifically hybridises to a gene listed in the specification, a computer
 CC system comprising a database containing information identifying the
 CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
 CC set of genes comprising at least two genes listed in the specification,
 CC and a user interface to view the information used to present information
 CC identifying the expression level in a tissue or cell of at least one gene
 CC listed in the specification. The method is useful for elucidating global
 CC changes in gene expression and for identifying toxicity markers in
 CC tissues or cell exposed to a known toxin. The genes may be used as
 CC toxicity markers in drug screening and toxicity assays. The genes and
 CC gene expression information may be used as diagnostic markers for the
 CC prediction or identification of the physiological state of tissue or cell
 CC sample that has been exposed to a compound or agent. Hepatotoxicity
 CC is characterised by centrilobular necrosis and steatosis. The present
 CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
 CC which is differentially expressed in response to a hepatotoxic agent.
 XX
 SQ Sequence 654 BP; 214 A; 153 C; 159 G; 128 T; 0 other;
 Alignment Scores:
 Pred. No.: 1.89e-33 Length: 654
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 24 Gaps: 2
 US-10-031-403-1 (1-146) x ABR63445 (1-654)
 OY 1 MetAlaGlyLeuThrProGluAlaGlyLeuThrLysLysAlaPheSerAlaVal 20
 Db 112 ATGGCTGATGACTGACTGAGAACAGATGCTGATTCAGAGAGCTTCTCCCTATT 171
 OY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 Db 172 GATAAAGATGGGCGCGACCATCAACAAGAGAGCTGCGGACTGTCATCGGCTCACTG 231
 OY 41 GilyLysAsnLeuSerGluAlaGlnLeuArgLysLeuLysSerGluValAspSerAspGly 60
 Db 232 GGTGACAGAACCCAGACAGAGCTGAGATGATCAACGAGGTGATGCCGACGGC 291
 OY 61 AspGlyValLeuSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 Db 292 AATGGCACCTTGAATCTCCAGAGCTTGTGATGTGGTGAAGAAAATGAAGACACA 351
 OY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 Db 352 GATAGCGAAGAGAAATCCGTGAGCGCATTTGACAAAGATGCGCAATGCGCTAC 411

OY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117
 Db 412 ATCAGTCGGCGAGAACTGCGGCGGAGAAAGCTAAGACGATGAA 471
 OY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyValAspTyrGlu 137
 Db 472 GAAGTACAGCAAAATGATCAAGAGAAAGATATGATGAGACGAGAGTCAACTATGAA 531
 OY 138 GluPheAlaArgMetLeu 143
 Db 532 GAATTCGTACAGATGATG 549

Search completed: May 16, 2003, 03:47:52
 Job time : 254 secs

QY 1 MetAlaGlyGluLeuThrProGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
 DB 58 ATGGCGTACAGCTGACTGAGAGAGATGCGAGATTCAGAGAGCCCTTCCCTTT 117
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 DB 118 GACAAGGATGAGATGGCTACTACACCAAGAGAGTGGGCACTGATGATGATCCCTG 177
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluAlaLysPheAspGly 60
 DB 178 GACACAGAACCCCACTGAACAGAGCTGCGAGATATGATCAATGAGTGGATGCGATGG 237
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 DB 238 AACGGACCATTCGATCCCGGAGTTCCTGACCATGATGGCCAGAAAGTGAAGACACA 297
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 DB 298 GACAGTGAAGAGAGATCCGAGAGAGCGCTTCCTTGTACAAAGATGGAGATGGCTAC 357
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117
 DB 358 ATCAGCGCCGCAAGCTGCGTCACTAATGACCAACCTGGGAGAGCTGACCGATGAG 417
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGlu 137
 DB 418 GAGGTGAGATGATGATGATGAGGAGGCTGACATGATGATGATGATGATGATGATGAA 477
 QY 138 GluPheAlaArgMetLeu 143
 DB 478 GAGTTGTACAGATGATG 495
 RESULT 14
 AA004332
 ID AA004332 standard; DNA; 654 BP.
 AC AA004332;
 XX
 DT 27-SEP-1990 (first entry)
 XX
 DE Plasmid pRCM1 and gene for construction of calmodulin expression vector.
 XX
 KW Calmodulin; ds.
 XX
 OS Rattus rattus.
 XX
 PN -UP02092286-A.
 XX
 PD 03-APR-1990.
 XX
 PF 30-SEP-1988; 88JP-0246239.
 XX
 PR 30-SEP-1988; 88JP-0246239.
 XX
 PA (KIRI) KIRIN BREWERY KK.
 XX
 DR WPI; 1990-144900/19.
 XX
 PT Calmodulin prepn. - by culturing transformed E. coli.
 XX
 PS Disclosure; ; P; Japanese.
 XX
 CC The plasmid is cut with HindIII and XbaI and inserted into a cloning
 CC site in pCALM1. The resulting plasmid, pCALM7 can be cut and ligated
 CC to Affili/BamHI cut pST6311 to produce the expression plasmid pTCAL7.
 CC See also AA004331-4.
 XX
 SQ Sequence 654 BP; 214 A; 153 C; 159 G; 128 T; 0 other;

Alignment Scores: 1.89e-33 Length: 654
 Pred. No.: 384.50 Matches: 76
 Score:

Percent Similarity: 73.97%
 Best Local Similarity: 52.05%
 Query Match: 52.74%
 DB: 11
 Gaps: 2

US-10-031-403-1 (1-146) x AA004332 (1-654)

QY 1 MetAlaGlyGluLeuThrProGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
 DB 112 ATGGCGTACAGCTGACTGAGAGAGATGCGAGATTCAGAGAGCCCTTCCCTATT 171
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 DB 172 GATAAAGATGGGACGCGCACATCACAAAGAGAGCTGGGCACTGCTCATGCGCTCAC 231
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluAlaLysPheAspGly 60
 DB 232 GGTCAAGAACCCCAAGAGCTGAACTGACAGATATGATCAACGAGTGGATGCGACGG 291
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 DB 292 AATGGACCATTCATCTCCAGAGTTCCTGACATGATGCTGAAAGTGAAGACACA 351
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 DB 352 GATAGCGAAGAAAGATCCGTGAGCGATTCGAGTCTTGACAAAGATGGCAATGGCTAC 411
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117
 DB 412 ATCAGTGGCGCAAGCTGCGCACGTCATGACAAACCTGGGAGAGAGCTGAACAGATGAA 471
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGlu 137
 DB 472 GAGGTGAGATGATGATGATGAGGAGGCTGACATGATGATGATGATGATGATGATGAA 531
 QY 138 GluPheAlaArgMetLeu 143
 DB 532 GATTCGTACAGATGATG 549
 RESULT 15
 ABR63445
 ID ABR63445 standard; cDNA; 654 BP.
 AC ABR63445;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Rat sequence differentially expressed in response to a hepatotoxin #1352.
 XX
 KW Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
 KW differential expression; centrillobular necrosis; steatosis.
 XX
 OS Rattus norvegicus.
 XX
 PN W0200210453-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 30-JUL-2001; 2001WO-US23872.
 XX
 PR 31-JUL-2000; 2000US-222040P.
 PR 02-NOV-2000; 2000US-244880P.
 PR 11-MAY-2001; 2001US-290029P.
 PR 15-MAY-2001; 2001US-290645P.
 PR 22-MAY-2001; 2001US-292336P.
 PR 06-JUN-2001; 2001US-295798P.
 PR 13-JUN-2001; 2001US-297457P.
 PR 19-JUN-2001; 2001US-298884P.
 PR 09-JUL-2001; 2001US-303459P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Mendrick D, Porter MM, Johnson KR, Castle AL, Elashoff MR;

Db 404 GAACTGATGAATGATCAGGAGACAGATATTGATGTCATGCTCAAGTAACATATGAA 463
 QY 138 Gluphealarqmetleu 143
 ||||| :|||:
 Db 464 GAGTTTGTACAAATGATG 481
 RESULT 12
 AAQ04334
 ID AAQ04334 standard; DNA; 504 BP.
 AC AAQ04334;
 XX
 DT 27-SEP-1990 (first entry)
 XX
 DE Plasmid pOCAL7 contg. gene for calmodulin.
 XX
 KM Calmodulin; ds.
 XX
 OS Rattus rattus.
 XX
 PN JP02092286-A.
 XX
 PD 03-APR-1990.
 XX
 PF 30-SEP-1988; 88JP-0246239.
 XX
 PR 30-SEP-1988; 88JP-0246239.
 XX
 PA (KIRI) KIRIN BREWERY KK.
 XX
 DR WPI; 1990-144900/19.
 XX
 PT Calmodulin prepn. - by culturing transformed E. coli.
 XX
 PS Disclosure; P; Japanese.
 XX
 CC The plasmid, pOCAL7, can be cut out and ligated to AflII/BamHI cut
 CC pST6311 to produce the expression plasmid pTCAL7.
 CC See also AAQ04331-3.
 XX
 SQ Sequence 504 BP; 170 A; 102 C; 131 G; 101 T; 0 other;
 Alignment Scores:
 Pred. No.: 1,38e-33 Length: 504
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 11 Gaps: 2
 US-10-031-403-1 (1-146) x AAQ04334 (1-504)
 QY 1 MetAlaGlyLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
 ||||| :|||:
 Db 17 ATGGCAGATCAATTACACAGAGAAACAGATCGCTCAATTCAAAGAGCTTTCTCCCTATT 76
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnLeuGluAlaAlaLeuLysAlaThr 40
 ||| :|||:
 Db 77 GATTAAGATGTGGACGCGACCATCACAAAGAGAGCTGGGACTGTCATGCGGTCCTG 136
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValaLysPheSerAspGly 60
 ||||| :|||:
 Db 137 GGTACAGAACCCACAGAGGTGTAAGTCAAGATATGATCAACGAGTGATGCCGACGGG 196
 QY 61 AspGlyLeuIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 :||| :|||:
 Db 197 AATGGCAGCATTTGACTCCAGAGTTCTTACTATGATGCTAGAAAAGAAAGACACA 256
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaAlaPheArgAlaPheAspGlnAspGlyHis 97
 ||||| :|||:
 Db 257 GATAGCAGCAAGAGAAATCCGTGAGGCAATCCGAGTCTTTGACAAAGATGCAATGCGCTAC 316
 QY 98 IleThrValaspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117

Db 317 ATCAGTCGGCAGAACTGCCACAGCTCATGACAAACCTCGGGGAAAGCTAACAGATGAA 376
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValaLysPheGlyAsnValaSerTyrGlu 137
 ||||| :|||:
 Db 377 GAAGTAGCAGCAATGATCAAGAGAGATATGATGAGAGACGACGATCACTATGAA 436
 QY 138 Gluphealarqmetleu 143
 ||||| :|||:
 Db 437 GAATTCCTACAGATGATG 454
 RESULT 13
 AAC03838
 ID AAC03838 standard; cDNA; 564 BP.
 AC AAC03838;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 3836.
 XX
 KM Human: 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KM gene therapy; chromosome mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX
 PA (GEST) GENSET.
 XX
 DR Dumas Milne Edwards J, Duclert A, Giordano J;
 DR P-PSDB; AAC03832.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 Claim 1; SEQ ID 3836; 71pp + CD-ROM; English.
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. An ORF has been identified within the
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
 CC derived from 30 different tissues. EST sequences usually correspond
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
 CC well suited for isolating cDNA sequences derived from the 5' ends of
 CC mRNAs and even in those cases where longer cDNA sequences have been
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
 CC mRNAs with intact 5' ends and can therefore be used to obtain full length
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
 CC gene therapy and chromosome mapping procedures. They are used to obtain
 CC upstream regulatory sequences and to design expression and secretion
 CC vectors.
 SQ Sequence 564 BP; 146 A; 119 C; 191 G; 108 T; 0 other;
 Alignment Scores:
 Pred. No.: 1,58e-33 Length: 564
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 21 Gaps: 2
 US-10-031-403-1 (1-146) x AAC03838 (1-564)

CC using primers AA095551-3 to PCR amplify the coding region. The coding
CC region of the gene was inserted into the plasmids pMALiRTM-2, pIRp27
CC and pGEX-5X-1 to generate plasmids pMALiCAM (AA095550), pPICAM (AA095551)
CC and pGSTCAM (AA095552) respectively. These plasmids express maltose-
CC (AAR78524), protein A- (AAR78525) and
CC glutathione-S-transferase calmodulin (AAR78526) fusion proteins,
CC respectively. The fusion proteins produced retain the same activity as
CC calmodulin as measured by the phosphodiesterase activating method. The
CC fusion protein, which can be obtained at high purity, can be used to
CC isolate calmodulin binding proteins, measure their activity and screen
CC for calmodulin inhibitors.

Sequence 450 BP; 167 A; 61 C; 115 G; 107 T; 0 other;

Alignment Scores:

Pred. No.:	1,21e-33	Length:	4
Score:	384.50	Matches:	7
Percent Similarity:	73.9%	Conservative:	3
Best Local Similarity:	52.05%	Mismatches:	3
Query Match:	52.7%	Indels:	3
DB:	16	Gaps:	2

US-10-031-403-1 (1-146) x AAQ95549 (1-450)

QY	1	MetIlaaglygulteurProGIuGIuLaInIryLyLaIaphSerAlaVal	20
		: : : : : :	
Db	1	ATGGCTGACCAACTGACGTGAGACGACAGTTCCAGATTCCAAAGAGCTTTTCACTATT	60
QY	21	AspThrAspGlyasnGlyThrTLeasnAlaGlnGluLeuGlyAlaIaIaLeuLysAlaThr	40
		: : : : : :	
Db	61	GACAAAGATGTGTATGTAACATTAACAACAAAGGAATGGGAACTGTAAATGACATCTCTT	120
QY	41	GlyLysAsnLeuSerGluAlaGlnLeuAryLysLeuIleSerGluValaAspSerAspGly	60
		: : : : : :	
Db	121	GGCGCAATCCCAACAGACGAGATTTACGGACATGATTAATGAAAGTAGATGCTGATGCT	180
QY	61	AspGlyGluIleSerPheGlnGluPheLeuThr--AlaIaIaGlyLysAlaArg-----	77
		::: : : : : : : : : : : : : : :	
Db	181	AATGGCAACAATTGACTTCCTCGAATTTCTGTGACAAATGATGCGCAAGAAATAAGAACACACA	240
QY	78	AlaGlyLeuGlnAspLeuGlnValaIaIaPheArgAlaPheAspGlnAspGlyAspGlyHis	97
		: : : : : :	
Db	241	GACAGTGAAAGAAATTAAGAAAGCAATTCCTGTGTGTTGATTAAGATGGCAAAATGGCTAT	300
QY	98	IleThrValaIaSpGluLeuArgArgAlaMetValaGlyLeuGlyGlnProLeuProGlnGlu	117
		: : : : : :	
Db	301	ATTAGTGTGTGAGAACTTCCCATGTGTATGCAACAACTTGGAGCAAGATTAAACAGATGAA	360
QY	118	GluLeuAspAlaMetIleArgGluIaIaAspValaIaAspGlnAspGlyArgValaAsnTyrGlu	137
		: : : : : :	
Db	361	GAAATTGATGAATGAATCAGCAGGAAGCAAGATATATGATGTGTATGGTCAAGTAAACTATGAA	420
QY	138	GluPheAlaIaArgMetLeu 143	
		: : : : : :	
Db	421	GAGTTTGTACAAATGATG 438	

RESULT 11

ID	ABK44905	standard; CDNA; 485 BP
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

DT 05-JUN-2002 (first entry)

cdna encoding colon tumour protein, SEQ ID NO 456

KM Human; colon tumour; vaccine; colon cancer; immunogenic
KW immunotherapy; gene; ss.

OS Homo sapiens.

PN WO200212328-A2
XX

PD 14-FEB-2002

PF 31-JUL-2001; 2001WO-US24218

PR 03-AUG-2000; 2000US-223283P
PR 03-AUG-2001; 2001US-279763P

PR 29-JUN-2001; 200105-302031P
XX

(CONT.) CONTAIN CONF. :
 XX
 XX
 XX

[illegible]

XX

PT for diagnosing, preventing,

XX

XX

CC The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions such as vaccines for the treatment and

hybridisation probes or primers and in the design and preparation of

proteins in tumour cells. The compositions are useful for stimulating an

cc colon cancer, and as markers for the progression of

proteins of CC

CC Note: With the exception of SEQ ID No 1 and 2, the sequence data
CC for this patent did not form part of the printed specification but was
CC supplied by the European Patent Office.
XX
XX
SQ Sequence 485 BP; 168 A; 69 C; 130 G; 118 T; 0 other;

US-10-031-403-1 (1-146) X ABK44905 (1-485)

Oy	1	MetalArglyLeuThrProGlnIuLagInglyPylsAlaPheserAlaval	20
Dd	44	ATGGCTGCACCAACTGACTGAAGACGACGATGTCCAGAAATTCAAAAGAAGCTTTTCTACTATT.	109
Oy	21	AspThrAspGlyAsnGlyThrThrIleasnAlaGlnIuleugIalAlaLeuLyalaThr	40
Dd	104	GACAAGAATGTGTGATGAAGCATPTATAACAAAAAGGAATGGGAACTGTATAGATCTCTT	167
Oy	41	GlylvsAsnLeuSerGluAlaGlnIeuArtyglvSleuIlleserGlualaSpserApsply	60
Dd	164	GGCGCAGATCCCACGAAGAACGAGATTAACGAGACATGATATTAAGTAGATGATGATGGT	228
Oy	61	AspGIgylullieserPheGlnGluPheLeuthr---AlaIlaArglysAlaArg-----	77
Dd	224	AATGCCACAAATTGACTTCCCTCGAATTTCTGTCAATGTATGCGCACAAAAATGMAAGACACA	288
Oy	78	AlaGlyLeuGluuaSpIeugIvalAlaPheArtyglAlaPhasapGlnaSpGlyASPGLYHS	97
Dd	284	GACAGCTGAAGAANAATTAGCAAGCATTCCTGTGTGTTTAAGAATGGCAATGGCTAT	348
-Oy	98	IleThrValaspGluLeuArtyArgAlametaLaGlyLeuengIynProLeuProGlnIu..112	
Dd	344	ATTGATGTCTGCAGAACTCCGCCATGTGTATGCACAAACCCTTGAGAGAAAGTTAAcGATGAA	408
Oy	118	GluLeuAspAlaMetIleArgGluAlaAlaAspValaSpGlnAspGlyArtyglValaArtyglu	137

PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-488781/53.
 DR P-PSDB; AAM43549.
 XX
 PT New isolated nucleic acids and polypeptides, useful for diagnosing,
 PT treating and/or preventing human diseases and disorders -
 XX
 PS Claim 1; SEQ ID NO 63; 664pp + Sequence Listing; English.
 XX

CC The invention relates to human polynucleotides (AA163803-AA164012) and
 CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. The
 CC genes were isolated from a range of human tissues disclosed in the
 CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
 CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
 CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
 CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
 CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX

XX Sequence 920 BP; 197 A; 274 C; 313 G; 135 T; 1 other;

Alignment Scores:

Pred. No.:	1,79e-70	Length:	920
Score:	722.00	Matches:	144
Percent Similarity:	99.32%	Conservative:	1
Best Local Similarity:	98.63%	Mismatches:	1
Query Match:	99.04%	Indels:	0
DB:	22	Gaps:	0

US-10-031-403-1 (1-146) x AAI63855 (1-920)

OY 1 MetAlaGluLeuThrProGluGluGluAlaGluTyrTyrLysAlaPheSerAlaVal 20
 DB 137 ATGGCCGGGAGCTGACTCTCGAGAGAGAGCCCAATACAAAAGGCTTCTCCGGGTT 196
 OY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGluLeuGlyAlaIleuLysAlaThr 40
 DB 197 GACACGAGTGAAGACGACCATCATGCGCAGAGACTGGCGCGCGCGTGAAGGCACG 256
 OY 41 GlyValAsnLeuSerGluAlaGluLeuArgLysLeuIleSerGluValAspSerAspGly 60
 DB 257 GGCAGAACCTCTCGAGAGCCCACTAAGGAACTATCTCGAGGTTTGCACGCGGC 316
 OY 61 AspGlyGluIleSerPheGluGluPheLeuThrAlaAlaArgLysAlaThrGlyLeu 80
 DB 317 GACGGGAAATCAGCTTCAGAGGTTCTGACGCGCGCGCAAGAGGCCAGGCGCGCTG 376
 OY 81 GluAspLeuGluValAlaPheArgAlaPheAspGluAspGlyLysIleThrVal 100
 DB 377 GAGGACTCTCAGTGCCTTCGCGCTTCGACACAGATGGCGACGCGCACATCACCGTG 436
 OY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGluGluLeuAsp 120
 DB 437 GACGACTCTGCGGGCGCTGCGGGCGTGGCGCACCCCTCGCCGACGAGGAGCTCGAC 496
 OY 121 AlaMetIleArgGluAlaAspValAspGluAspGlyArgValAspTyrGluGluPheAla 140
 DB 497 GCCATGATCCGGAGGCGCAGCGTGGACAGAGCGGCGGTTGAATACGAGGAGTTCGCG 556

OY 141 ArgMetLeuAlaGlu 146
 DB 557 AGGATGCTCGCCAGGAG 574

RESULT 8

AAAF21853
 ID AAF21853 standard; DNA; 497 BP.

AC AAF21853;

DT 27-MAR-2001 (first entry)

XX Human breast and ovarian cancer associated antigen gene SEQ ID 240.

XX Human; breast cancer; cytostatic; immunosuppressive;
 KW neurotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 KW antidiabetic; antiinflammatory; antitumor; antiviral; anticonvulsant;
 KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
 KW Addison's disease; allergy; diabetes mellitus; Crohn's disease;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease; ds.

XX Homo sapiens.

XX WO200055173-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000MO-US05881.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2000-611515/58.

XX P-PSDB; AAB58950.

PT New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention,
 PT treatment and diagnosis of cancer, immune disorders, cardiovascular
 PT disorders and neurological diseases -
 XX

PS Claim 1; Page 665; 1299pp; English.

CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic; immunosuppressive;
 CC neurotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 CC antidiabetic; antiinflammatory; antitumor; antiviral; anticonvulsant;
 CC antibacterial; antifungal; antiparasitic and cardiant activity. The
 CC polynucleotide and protein sequences are used in the diagnosis of cancer,
 CC particularly breast and ovarian cancer. The nucleic acid sequences,
 CC proteins, agonists and agonists may also be used in the diagnosis,
 CC prevention and treatment of immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; cardiovascular disorders such as
 CC myocardial ischaemia; wound healing; neurological diseases such as
 CC cerebral anoxia and epilepsy; and infectious diseases.

XX Sequence 497 BP; 100 A; 143 C; 176 G; 70 T; 8 other;

Alignment Scores:

Pred. No.:	1,61e-49	Length:	497
Score:	529.00 <td>Matches:</td> <td>107 </td>	Matches:	107
Percent Similarity:	96.40%	Conservative:	0

KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KM cardiovascular disorder; neurological disease; infection; human; ss.
XX Homo sapiens.
XX WO200155308-A2.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US01309.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186330.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.

PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.

PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246174.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246533.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249267.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 DR WPI: 2001-581633/65.
 DR P-PSDB: AAU87578.
 XX
 PT New isolated nucleic acid encoding a protein for diagnosing,
 PT preventing, treating or ameliorating medical conditions and used as
 PT food additives or preservatives -
 XX
 PS Claim 1; SEQ ID NO 498; 837bp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule (I) encoding a
 CC novel central nervous system protein. (I) and polypeptides (III) encoded
 CC by (I), are used to treat a medical conditions and in diagnosis of a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and

CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
 CC adenocarcinomas and irritable bowel syndrome, reproductive system
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 CC leukemia, disorders involving neovascularisation e.g. malignancies,
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 CC acute kidney failure and blood related disorders e.g. myocardial
 CC infarction. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,

Alignment Scores:
 Pred. No.: 1,71e-70 Length: 884
 Score: 722.00 Matches: 144
 Percent Similarity: 99.32% Conservative: 1
 Best Local Similarity: 99.63% Mismatches: 1
 Query Match: 99.04% Indels: 0
 Db: 23 Gaps: 0

US-10-031-403-1 (1-146) x ABK43908 (1-884)
 QY 1 MetAlAGlGluLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
 Db 135 ATGGCCGGTAGCTGACTCTCTGAGAGAGAGGCCCAATCAAAAGGCTTCTCCGGCTT 194
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleuLysAlaThr 40
 Db 195 GACACGAGTGAAGAAAGCAGCACCATCAATGCCACAGAGCTGGCCGCGCTGAAGGCCACG 254
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 255 GGCAGAACCTCTCGAGAGGCCAGCTAAGAACTATCTCCAGGTTCACRGGACGGC 314
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
 Db 315 GACGGCGAAATCAGCTTCCAGAGGTTCTTACGCGCGCGGCGAAGAGCCAGCGCGCTG 374
 QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyLysIleThrVal 100
 Db 375 GAGGACCTCGAGGTCCCTCCGCGCTTCGACAGAGATGGCGACGCCACATCACCGT 424
 QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluLeuAsp 120
 Db 435 GACGAGCTCAGCGCGGCATGGCGGGCTGGGGCAGCCGCTGCCGAGGAGAGCTGGAC 494
 QY 121 AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGlnGluPheAla 140
 Db 495 GCCATATCCGCGAGGCCGACGCTGGACACAGAGCGGGGTGAATCAACAGAGATTCCGC 554
 QY 141 ArgMetLeuAlaGlnGlu 146
 Db 555 AGGATGCTCGCCACGAGAG 572

RESULT 7
 AA163855
 ID AA163855 standard; cDNA; 920 BP.
 XX
 AC AA163855;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 63.
 XX
 KW Human; antiarthritis; antirheumatic; antiproliferative; vasotropic;
 KW cerebroprotective; nootropic; neuroprotective; antibacterial; vinnocic;
 KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
 KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
 KW antiinflammatory; antilucer; vulnerary; anticonvulsant; antibacterial;

QY 1 MetAlaGlyLeuThrProGluGluGluAlaGlnTrpLysLysAlaPheSerAlaVal 20
|
Db 135 ATGGCCGCTAGCTGACTCTCTGAGAGAGAGCCAGTACAAAAAGCTTCTCCGCGTT 194
|
QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
|
Db 195 GACACGATGGAAGACGGACCATCAATGCCAGAGCTGGGGCGGCTGAAGGCCACG 254
|
QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
|
Db 255 GGCAGAACCTCTCGAGGGCCAGCTAAGAACTCATCTCCGAGTTGACRGGAGCGC 314
|
QY 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
|
Db 315 GACGGCAAAATCAAGCTTCCGAGATTCTCAGCGCGCGAAGAGCGCGGCGCTG 374
|
QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
|
Db 375 GAGGACCTGCAGGTCCCTTCCGCGCTTGCACAGATGGCGGCGCACATCACCGTG 434
|
QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluLeuAsp 120
|
Db - 435 GACGAGCTCAGCGCGGCGCATGCGGGCGCTGGCGAGCGCGTCCCGCAGAGAGACTGGAC 494
|
QY 121 AlaMetIleArgGluAlaAspValAlaAspGlnAspGlyArgValAsnTrpGluGluPheAla 140
|
Db 495 GCCATGATCCGCGAGCGCGAGCTGGACAGAGCGGGGTGAATCAAGAGATTGCGC 554
|
QY 141 ArgMetLeuAlaGlnGlu 146
|
Db 555 AGGATGCTGCCCGCAGGAG 572
|
RESULT 6
ABK43908
ID ABK43908 standard; cDNA; 884 BP.
XX
AC ABK43908;
XX
DT 05-JUN-2002 (first entry)
XX
DE DNA encoding novel central nervous system protein #488.
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200155318-A2.
XX
PD 02-AUG-2001.
PF 17-JAN-2001; 2001MO-US01332.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216680.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 14-AUG-2000; 2000US-0226279.
PR 18-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 29-SEP-2000; 2000US-0236379.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.

PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0228287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 06-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 08-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0233397.
 PR 14-SEP-2000; 2000US-0233398.
 PR 14-SEP-2000; 2000US-0233399.
 PR 14-SEP-2000; 2000US-0234400.
 PR 14-SEP-2000; 2000US-0234401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235844.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.

PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259676.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI: 2001-465568/50.
 P-PDB: AAU19929.

Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition -
 Claim 4; SEQ ID No 48; 542pp; English.

The present invention relates to the isolation of novel human calcium-binding proteins (AAU19892-AAU19969), and cDNA and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amyotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID), digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. hemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AAS31577-AAS31634 represent cDNA sequences encoding for the novel human calcium-binding proteins.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 884 BP; 162 A; 273 C; 311 G; 135 T; 3 other;

Alignment Scores:
 Pred. No.: 1,71e-70 Length: 884
 Score: 722.00 Matches: 144
 Percent Similarity: 99.32% Conservative: 1
 Best Local Similarity: 98.63% Mismatches: 1
 Query Match: 99.04% Indels: 0
 DB: 22 Gaps: 0

US-10-031-403-1 (1-146) x AAS31614 (1-884)

Db	375	GAGGACCTGCAGGTCGGCTTCCGGCGCTTGACACAGATGGCGACGGCACATCACC	43
QY	101	AspeltuleuargargalaMetalaGlyLeuGlycProleuProGingluGluLeuAsp	120
DG	435	GACACAGCTCAGCGCGGCATCGCGGGCTGGCGCAGCCGCTGCCGACGAGGACCTGGAC	494
QY	121	AlaMetileuargguAlaAspValaAspGlnaAspGlyArgValaAsnTYrGluGluPheAla	140
Db	495	GCCATGATCCCGCGAGGCCGACGCTGGACAGACAGACGCGGGGTGAACCTACGAGAGTTCCGC	554
QY	141	ArgMetLeuAlaGlnGlu	146
Db	555	AGGATGCTCGCCACGAG	572
RESULT 5			
AAS31614			
ID	AAS31614 standard; cDNA; 884 BP.		
XX			
AC			
XX			
XX	AAS31614;		
DT			
DT	04-DEC-2001 (first entry)		
DE	cDNA encoding novel human calcium-binding protein #38.		
XX			
KW	Human; calcium-binding protein; calcium flux; neurological disease;		
KW	immune dysfunction; digestive disorder; neoplastic disease;		
KW	blood disorder; infectious disease; gene therapy; immunosuppressive;		
KW	antiarthritic; cyostatic; vasotropic; antibacterial; nootropic;		
OS	vitruclide; ss.		
XX			
XX	Homo sapiens.		
PN			
XX	WO200155304-A2.		
PD			
XX	02-AUG-2001.		
XX			
PF	17-JAN-2001; 2001MO-US01392.		
XX			
PR	31-JAN-2000;	2000US-0179065.	
PR	04-FEB-2000;	2000US-0180628.	
PR	24-FEB-2000;	2000US-0184664.	
PR	02-MAR-2000;	2000US-0186350.	
PR	16-MAR-2000;	2000US-0189874.	
PR	17-MAR-2000;	2000US-0190076.	
PR	18-APR-2000;	2000US-0198123.	
PR	19-MAY-2000;	2000US-0205515.	
PR	07-JUN-2000;	2000US-0209467.	
PR	28-JUN-2000;	2000US-0214886.	
PR	30-JUN-2000;	2000US-0215135.	
PR	07-JUL-2000;	2000US-0216647.	
PR	07-JUL-2000;	2000US-0216880.	
PR	11-JUL-2000;	2000US-0217487.	
PR	11-JUL-2000;	2000US-0217496.	
PR	14-JUL-2000;	2000US-0218290.	
PR	26-JUL-2000;	2000US-0220963.	
PR	26-JUL-2000;	2000US-0220964.	
PR	14-AUG-2000;	2000US-0224518.	
PR	14-AUG-2000;	2000US-0224519.	
PR	14-AUG-2000;	2000US-0225213.	
PR	14-AUG-2000;	2000US-0225214.	
PR	14-AUG-2000;	2000US-0225267.	
PR	14-AUG-2000;	2000US-0225267.	
PR	14-AUG-2000;	2000US-0225268.	
PR	14-AUG-2000;	2000US-0225270.	
PR	14-AUG-2000;	2000US-0225447.	
PR	14-AUG-2000;	2000US-0225757.	
PR	14-AUG-2000;	2000US-0225758.	
PR	14-AUG-2000;	2000US-0225759.	
PR	18-AUG-2000;	2000US-0226279.	
PR	22-AUG-2000;	2000US-0226681.	
PR	22-AUG-2000;	2000US-0226868.	
PR	22-AUG-2000;	2000US-0227182.	
PR	23-AUG-2000;	2000US-0227009.	

XX 22-OCT-2001 (first entry)
XX Human polynucleotide SEQ ID NO 141.
DE
XX
KV Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KV cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KV fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KV neuroprotective; antiatheric; hepatotropic; antidiabetic;
KV antiinflammatory; antitumor; anticonvulsant; antibacterial;
KV antiparasitic; cardiac; gene therapy; cancer; immune disorder;
KV cardiovascular disorder; neurological disease; infection; human; ss.
XX
XX Homo sapiens.
XX
XX MO20015308-A2.
XX
XX 02-AUG-2001.
XX
XX
XX 17-JAN-2001; 2001WO-US01309.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 02-MAR-2000; 2000US-0184664.
XX 16-MAR-2000; 2000US-0186350.
XX 17-MAR-2000; 2000US-0189874.
XX 18-APR-2000; 2000US-0190076.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 11-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 14-JUL-2000; 2000US-0217496.
XX 26-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225267.
XX 14-AUG-2000; 2000US-0225268.
XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226868.
XX 22-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227109.
XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 01-SEP-2000; 2000US-0229345.
XX 05-SEP-2000; 2000US-0229509.
XX 06-SEP-2000; 2000US-0230437.
XX 06-SEP-2000; 2000US-0230438.
XX 08-SEP-2000; 2000US-0231242.
XX 08-SEP-2000; 2000US-0231243.
XX 08-SEP-2000; 2000US-0231244.
XX 08-SEP-2000; 2000US-0231413.
XX 08-SEP-2000; 2000US-0231414.
XX 08-SEP-2000; 2000US-0232080.
XX 08-SEP-2000; 2000US-0232081.
XX 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0233397.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233400.
PR 14-SEP-2000; 2000US-0233401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241285.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.

02-OCT-2000; 2000US-0237039.
 PR 13-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241281.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249287.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 01-DEC-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 01-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-581633/65.
 DR P-PSDB; AAU87283.
 XX
 PT New isolated nucleic acid encoding a protein for diagnosing,
 PT preventing, treating or ameliorating medical conditions and used as
 PT food additives or preservatives -
 XX

PS Claim 1; SEQ ID No 203; 837bp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule (I) encoding a
 CC novel central nervous system protein. (I) and polypeptides (III) encoded
 CC by (I), are used to treat a medical conditions and in diagnosis of a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
 CC adenocarcinomas and irritable bowel syndrome, reproductive system
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 CC leukemia, disorders involving neovascularisation e.g. malignancies,
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 CC acute kidney failure and blood related disorders e.g. myocardial
 CC infarction. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,

Alignment Scores:

Pred. No.:	6,79e-71	Length:	955
Score:	726.00	Matches:	145
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.32%	Mismatches:	0
Query Match:	99.59%	Indels:	0
DB:	23	Gaps:	0

US-10-031-403-1 (1-146) x ABK43613 (1-955)

QY	1	MetlaelgtyleuthrproglugluuAaInlrylsyAaIapheserAlaVal	20
DB	136	ATGGCCGGTGAAGTCTCGAGAGAGCCAGTACAAAGCGCTTCTCCGCGTT	195
QY	21	AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIaLeuLysAlaThr	40
DB	196	GACACGGATGAAGGCGACCATATATGCCAGAGCTGGCGCGGCTTAAGGCCACG	255
QY	41	GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly	60
DB	256	GGCAAGAACTCTGGAGGCCACCTAAGAACTCATCTCCGAGTTGACAGCGAGCGC	315
QY	61	AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaIaGlyLeu	80
DB	316	GACGGCGAAATCACCTTCAGAGAGTCTTCAGCGCGGCGAAGAGCGGCGGCGCTG	375
QY	81	GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyLysIleThrVal	100
DB	376	GAGAGCTCGAGTCCGCTTCGCGCTTCGACAGATGCGCGCCACATACCGCTG	435
QY	101	AspGluLeuArgArgAlaMetAlaGlyLeuGlyLeuProLeuProGlnGluLeuAsp	120
DB	436	GACAGAGCTCAGCGCGGCGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	495
QY	121	AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnIleGluGluPheAla	140
DB	496	GCCATGTATCCGCGAGCGGAGTGGACAGAGCGGCGGTTGAATCTAGAGGAGTTCGCG	555
QY	141	ArgMetLeuAlaGlnGlu	146
DB	556	AGATGCTCCGCCGAGAG	573

RESULT 4
 AA163933
 ID AA163933 standard; cDNA; 884 BP.
 XX
 AC AA163933;

Alignment Scores:
Pred. No.: 5,93e-71 Length: 853
Score: 726.00 Matches: 145
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.328 Mismatches: 0
Query Match: 99.59% Indels: 0
DB: 21 Gaps: 0

US-10-031-403-1 (1-146) x AAA10473 (1-853)

QY 1 MetAlaGlyLeuThrProGluGluGluAlaGlnTyrIlysAlaPheSerAlaVal 20
|||
DB 121 ATGGCCGGTGAAGCTCTGAGGAGGAGCCAGTACAAAAAGCTTCTCCGGGTT 180
|||
QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluGluGluAlaLeuLysAlaThr 40
|||
DB 181 GACACGATGGAACGGCCACCATCATGCCAGAGAGTGGCCGGCGGTGAAGGCCAGC 240
|||
QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluAlaAspSerAspGly 60
|||
DB 241 GCCAAGAACCTCTCGAGGCCAGCTAAGGAACCTATCTCCGAGGTGACAGCAGCGC 300
|||
QY 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
|||
DB 301 GACGGCGAAATCAAGCTTCCAGGAGTCTGACGGCGGCGGAAGGCCAGCGCGGCTG 360
|||
QY 81 GluAspGluGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
|||
DB 361 GAGGACCTGAGGTCCCTTCCGCGCTTGCACAGAGATGGCCACGCCATCACCCTG 420
|||
QY 101 AspGluLeuArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluGluLeuAsp 120
|||
DB 421 GACGACCTGAGGGCGGCGCAATGCGGGGCTGGGCGACCCGCTGCCGAGGAGAGCTGGAC 480
|||
QY 121 AlaMetIleArgGluAlaAspValaAspGlyArgValaAsnIlyGluGluPheAla 140
|||
DB 481 GCCATATCCGCGAGCGCCGAGTGGACAGGAGGGGGGTGAATCAGGAGGATTGCGC 540
|||
QY 141 ArgMetLeuAlaGlnGlu 146
|||||
DB 541 AGGATGCTGCGCCAGAG 558
|||||

RESULT 3
ABK43613
ID ABK43613 standard; cDNA; 955 BP.
XX
AC ABK43613;
XX
XX
DT 05-JUN-2002 (first entry)
XX
XX
DE DNA encoding novel central nervous system protein #193.
XX
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy; gene; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN MO200155318-A2.
PD
XX
XX
PD 02-AUG-2001.
XX
XX
PF 17-JAN-2001; 2001MO-US01332.
XX
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0229824.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234297.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.

FT CDS 114..554
 FT /*tag= a
 FT /product= "calmodulin-like skin protein"
 PN FR2796646-A1.
 XX
 XX
 PD 26-JAN-2001.
 XX
 XX 23-JUL-1999; 99FR-0009615.
 XX
 XX 23-JUL-1999; 99FR-0009615.
 XX
 XX (OREA) L'OREAL SA.
 XX
 XX Mehul B, Bernard D, Simonetti L;
 PI WPI: 2001-184569/19.
 XX P-PSDB: AAB67650.
 DR
 XX
 XX New polypeptide isolated from human skin and having calcium fixing
 PT activity, useful for regulating epidermal proliferation and
 PT differentiation, e.g. in treatment of dry skin, psoriasis or neoplasia
 PT
 PS Claim 17; Page 22; 28pp; French.
 XX
 XX The present sequence encodes a human calmodulin-like skin protein
 CC (CISP). CISP is a calcium-mediated signal pathway modulator. CISP
 CC polypeptides and polynucleotides are used cosmetically for regulating
 CC dysfunction of epidermal proliferation or differentiation (normal or
 CC pathological) and for treating dry skin, hyperkeratosis, parakeratosis,
 CC psoriasis, ichthyosis or neoplasia. They are especially used for
 CC treating skin aging and skin damage caused by exposure to ultraviolet
 CC radiation. They are also useful for preparing or purifying specific
 CC binding partners, especially specific antisera or monoclonal antibodies.
 CC
 XX
 SQ Sequence 858 BP; 155 A; 267 C; 301 G; 135 T; 0 other:
 Alignment Scores:
 Pred. No.: 2,79e-71 Length: 858
 Score: 729.00 Matches: 146
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-10-031-403-1 (1-146) x AAF55621 (1-858)
 QY 1 MetAlaGlyLeuThrProGluGluAlaGlnTrpLysLysAlaPheSerAlaVal 20
 DB 114 ATGGCCGGTGGAGTCTGCTCTGAGGAGAGGCCAGTACAAAGGCTTCTCCGGCGTT 173
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluGlyAlaIleLeuLysAlaThr 40
 DB 174 GACACGGATGGAAACGGCACCATCAATGCCAGAGGCTGGCGGCGCTTAAGGCGACG 233
 QY 41 GLyAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 DB 234 GGCAGAAAGCTCTCGAGAGGCCAGCTAAGAAACTCATCTCCGAGGTTGACAGGAGCGC 293
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaGlyLysAlaArgAlaGlyLeu 80
 DB 294 GACGGCGGAAACCATCTCCAGAGCTTCTGAGCGGCGGCAAGAGCGCGGCGCTG 353
 QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
 DB 354 GAGAGACTGCGAGTCCCTTCCGGCCCTTCGACAGAGATGGCGAGCGCATCATCCTG 413
 QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGluGluLeuAsp 120
 DB 414 GACGAGCTCAGCGGGCGCATGCGCGGGCTGGGCGAGCCGCTGCCAGAGAGAGCTGGAC 473
 QY 121 AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTrpGluGluPheAla 140

DB 474 GCCATGATCCGCGGAGCGGCGAGTGGACGAGCGGGGTGAATCACTGAGGAGTTCGCG 533
 QY 141 ArgMetLeuAlaGlnGlu 146
 DB 534 AGGATGCTCGGCCGAGGAG 551
 RESULT 2
 ID AAA10473 standard; cDNA; 853 BP.
 XX
 XX AAA10473:
 AC
 XX 18-JUL-2000 (first entry)
 DT
 XX
 XX cDNA encoding human disease-associated calmodulin protein (DACP-1).
 DE
 XX Disease-associated calmodulin protein; DACP-1; human; EF-hand;
 KW detection; quantitation; diagnosis; cancer; immune disorder;
 KW reproductive disorder; gynaecological; gene therapy; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT CDS 121..561
 FT /*tag= a
 FT /product= "Human DACP-1"
 PN US6046315-A.
 XX
 XX 04-APR-2000.
 PD
 XX
 XX 03-NOV-1997; 97US-0963409.
 PF
 XX 03-NOV-1997; 97US-0963409.
 PR
 XX 03-NOV-1997; 97US-0963409.
 XX
 XX (INCYT) INCYTE PHARM INC.
 PA
 XX Hillman J, Corley NC, Shah P;
 PI WPI: 2000-282708/24.
 DR P-PSDB: AAB7548.
 XX
 XX New polynucleotide encoding a disease associated calmodulin protein
 PT (DACP-1) useful for diagnosing, preventing and treating cancer, immune
 PT disorders and reproductive disorders
 PT
 PS Claim 4; Fig 1A-C; 27pp; English.
 XX
 XX This sequence represents cDNA encoding human disease-associated
 CC calmodulin protein (DACP-1). cDNA sequences encoding DACP-1 were
 CC initially isolated from a breast tumour cDNA library, this sequence
 CC being a consensus. Human DACP-1 has four EF-hand calcium-binding
 CC domains, and has chemical and structural homology with other calmodulin
 CC proteins from human, rat and Plasmodium falciparum. DACP-1 proteins and
 CC nucleotides are useful for the diagnosis, prevention, or treatment of
 CC cancers, immune disorders (e.g., AIDS) and reproductive disorders,
 CC including endometriosis. DACP-1 nucleotides are useful for detecting and
 CC quantitating gene expression in biopsied tissues in which expression of
 CC the protein may be correlated with a disease. Such a diagnostic assay may
 CC be used to distinguish between absence, presence, and overexpression of
 CC DACP-1, and to monitor regulation of DACP-1 levels during therapeutic
 CC intervention. The nucleotide sequences are also useful in assays used to
 CC evaluate the efficacy of a particular therapeutic treatment regimen in
 CC animal studies, in clinical trials, or in monitoring the treatment of an
 CC individual patient. Nucleotides encoding DACP-1 are also useful in
 CC modulating DACP-1 expression e.g., in antisense therapy. DACP-1, and
 CC DACP-1 fragments and antibodies may be used in drug screening techniques.
 CC The antibodies may also be useful for the diagnosis of diseases
 CC associated with abnormal DACP-1 expression or activity.
 XX
 XX Sequence 853 BP; 150 A; 270 C; 303 G; 130 T; 0 other;

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 16, 2003, 02:34:02 ; Search time 243 Seconds

(without alignments)
1353.052 Million cell updates/sec

Title: US-10-031-403-1

Perfect score: 729
Sequence: 1 MAGELTPEEAAQYKKAFAV.....DVDQDGRVNYEEFAFMIAQE 146

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/sgn2.1/USPRO.spool/US10031403/runat_08052003.131923.5671/app_query.fasta_1.327
-DB=N_Geneseq_101002 -QFMT=fastp -SUFFIX=ring -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Diosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10031403.ecgn.1.1.263.0runat.08052003.131923.5671 -NCPU=6 -ICPU=3
-NO.XLPXY -NO.MMAP -LARGESOURCE -NEG.SCORES=0 -MATT=LONGLOG -CPU=TIMOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	729	100.0	858	22	AAE55621	Nucleotide sequenc
2	726	99.6	853	21	AAA10473	cDNA encoding huma
3	726	99.6	955	23	ABK43613	DNA encoding novel
4	722	99.0	884	22	AAI63933	Human polynucleoti
5	722	99.0	884	22	AAI63933	cDNA encoding nove
6	722	99.0	884	22	ABK43908	DNA encoding novel
7	722	99.0	920	22	AAI63855	Human polynucleoti
8	529	72.6	497	21	AAE21853	Human breast and o
9	384.5	52.7	447	11	AAO04331	Recombinant calmod
10	384.5	52.7	450	16	AAO95549	Human calmodulin c
11	384.5	52.7	485	21	ABK44905	cDNA encoding colo
12	384.5	52.7	504	11	AAO04334	Plasmid pOCAL7 con
13	384.5	52.7	564	21	AAO03838	Human secreted pro
14	384.5	52.7	654	11	AAO04332	Plasmid pRCM1 and
15	384.5	52.7	654	24	ABK63445	Rat sequence diffe
16	384.5	52.7	1131	11	AAO05826	Human calmodulin g
17	384.5	52.7	1361	24	ABT99274	Mouse ischaemic co
18	384.5	52.7	2175	24	ABK83767	Human cDNA differe
19	384.5	52.7	2247	22	AAI44950	cDNA encoding nove
20	380.5	52.2	739	23	ABL20145	Drosophila melanog
21	380.5	52.2	995	23	ABL14119	Drosophila melanog
22	380.5	52.2	1049	23	ABL20141	GST-calmodulin fus
23	380.5	52.2	1128	16	AAO95552	Rat calmodulin enc
24	379.5	52.1	447	24	ABN83905	Protein A-calmodul
25	379.5	52.1	1230	16	AAO95551	Calcium binding pr
26	379.5	52.1	1608	16	AAO95550	Calcium sensor G85
27	376.5	51.6	1251	24	ABN83907	Fluorescent calmod
28	376.5	51.6	1929	19	AAV58275	Fluorescent calmod
29	376.5	51.6	1958	19	AAV58276	Fluorescent calmod
30	373.5	51.2	1929	19	AAV58277	Fluorescent calmod
31	373.5	51.2	1971	19	AAV58278	Human ovarian PC
32	371.5	51.0	624	22	AAI23941	Human ovarian PC
33	371.5	51.0	624	22	AAI23941	Human ovarian PC
34	371.5	51.0	624	22	AAI23941	Human ovarian PC
35	370.5	50.8	462	9	AAH80188	DNA encoding biosy
36	358.5	49.2	681	21	AAI10892	Human secreted pro
37	357.5	49.0	1306	24	ABL65422	Lung cancer relate
38	357.5	49.0	1306	24	ABL65422	Lung cancer relate
39	357.5	49.0	1306	24	ABL65422	Lung cancer relate
40	357.5	49.0	2746	24	ABL67803	Oesophagus cancer
41	355.5	48.8	672	24	ABO65821	Arabidopsis thalia
42	355.5	48.8	751	21	AAI33827	Arabidopsis thalia
43	355.5	48.8	906	17	AAI18078	Potato calmodulin
44	355.5	48.8	1133	20	AAI27544	Human ovarian tumo
45	352.5	48.4	456	21	AAI49319	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAE55621
AAE55621 standard; DNA; 858 BP.

29-MAY-2001 (first entry)

Nucleotide sequence of a human calmodulin-like skin protein.

Human; calmodulin-like skin protein; CLS; epidermal differentiation;

calcium-mediated signal pathway; epidermal proliferation; dry skin;

hyperkeratosis; parakeratosis; psoriasis; ichthyosis; neoplasia;

skin aging; skin damage; ss.

Homo sapiens.

Location/Qualifiers

Key

Alignment Scores:

Pred. No.:	1,08e-22	Length:	654
Score:	384.50	Matches:	76
Percent Similarity:	73.97%	Conservative:	32
Best Local Similarity:	52.05%	Mismatches:	35
Query Match:	52.74%	Indels:	3
DB:	6	Gaps:	2

US-10-031-403-1 (1-146) x E02315 (1-654)

```
OY 1 MetAlaGlyGluLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 112 ATGGCTGATCAGCTACTGACAGACAGATTCCTGAATTCAGAGAGCTTCTCCATTT 171
OY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
    ||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 172 GATTAAGATGGGGAGCGCACCATCAACAAGAGAGCTGGGACTGCTCATGGGTCACTG 231
OY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 232 GGTCAAGAACCCACAGAGAGCTGACTGCGATGATCAACAGAGTGATGCCAGCGG 291
OY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 292 AATGCACCATGACTCCACAGAGCTTCTGACTATGATGCTAAGAAAATGAAGACACA 351
OY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGluAspGlyHis 97
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 352 GATACCGAGAGAAATCCGTAGGCAATCCAGTCTTGACAGAGATGGCAATGGCTAC 411
OY 98 IleThrValAspGluLeuArgAlaIleAlaGlyLeuGlnProLeuProGlnGlu 117
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 412 ATCACTGGGGCGAGACTGGCCAGCTCATGACAAACCTGGGGAAGCTTAACAGATGAA 471
OY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGluAspGlyArgValAsnTyrGlu 137
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 472 GAAGTAGACGAATGATCAGAGACAGATATTGATGAGACGACAGAGTCAACTATGAA 531
OY 138 GluPheAlaArgMetLeu 143
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 532 GAATTCGTACAGATGATG 549
```

Search completed: May 16, 2003, 04:30:11
Job time : 2517 secs

US-10-031-403-1 (1-146) x AY046946 (1-622)

QY 1 MetAlaGlyGluLeuThrProGluGluAlaGlnGlyTyrLysAlaPheSerAlaVal 20
 DB 69 ATGGCTGATCAGCTGACGAGCAAGATTGCGAAATTCAGAACCTTTTCATATTT 128
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleLeuLysAlaThr 40
 DB 129 GACAAAGATGGTGAATGACATACACAAAGAAATTTGGAGCTGTAATGCGGTCTT 188
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 DB 189 GGGCAAAATCCACAGACAGAGATTACAGACATGATTAATGAGTAGATGCTGATGTT 248
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaIleArgLysAlaArg----- 77
 DB 249 AATGGCAACAATTCATCTCCCGAAATTTCTGACATGATGCGCAAGAAATGAAAGATACA 308
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 DB 309 GACAGTGAAGAAAGAAATTTAGAGAAAGATCCGCTGTTGATTAAGATGTTAATGGCTAT 368
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnGlnProLeuProGlnGlu 117
 DB 369 AATAGTGCAGCAGACAGCTCCGCTGATGATGACAAACCTTGAGAGAAATTAACAGATGAA 428
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGlu 137
 DB 429 GAGCTTGATCAATGATCAGGAGCAAGATATTGATGATGCTGATCAAGTAACTATGAA 488
 QY 138 GluPheAlaArgMetLeu 143
 DB 489 GAGTTGTACAAATGATG 506

RESULT 14
 AX401676 AX401676 654 bp DNA linear PAT 06-JUN-2002
 LOCUS Sequence 1352 from Patent WO0210453.
 DEFINITION AX401676
 ACCESSION AX401676
 VERSION AX401676.1 GI:21337856
 KEYWORDS

SOURCE

ORGANISM Norway rat.
 Rattus norvegicus

REFERENCE 1 Mendrick, D., Porter, M.W., Johnson, K.R., Castle, A.L. and
 AUTHORS Elashoff, M.R.
 TITLE Molecular toxicology modeling.
 JOURNAL Patent: WO 0210453-A 1352 07-FEB-2002;
 Gene Logic, Inc. (US)
 Ratus.

FEATURES
 source 1.654
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 /note="EMBL/GenBank Accession No. E02315"

BASE COUNT 214 a 153 c 159 g 128 t
 ORIGIN

Alignment Scores:

Pred. No.: 1.08e-22 Length: 654
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 6 Gaps: 2

US-10-031-403-1 (1-146) x AX401676 (1-654)

QY 1 MetAlaGlyGluLeuThrProGluGluAlaGlnGlyTyrLysAlaPheSerAlaVal 20
 DB 69 ATGGCTGATCAGCTGACGAGCAAGATTGCGAAATTCAGAACCTTTTCATATTT

DB 112 ATGGCTGATCAGCTGACGAGCAAGATTGCGAAATTCAGAACCTTTTCATATTT 171
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleLeuLysAlaThr 40
 DB 172 GATTAAGATGGGACGCGACCATCACAAAGAGCTGGGAGCTGTCAATGCGGTCACT 231
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 DB 232 GGTACAGAACCCACAGAGGCTGAATGACGATATGATCAACAGAGTGATGCTGCAGCGG 291
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaIleArgLysAlaArg----- 77
 DB 292 AATGGCAACAATTCATCTCCCGAAATTTCTGACATGATGCGCAAGAAATGAAAGATACA 351
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 DB 352 GATAGCAAGAAAGAAATTCCTGAGCATTCCTGATTCGATTAAGATGCGCATGCTAC 411
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnGlnProLeuProGlnGlu 117
 DB 412 ATCAGTCCGCGACAGACATGCGCCGCTGATGACAAACCTCGGAGAAAGCTTAACAGATGAA 471
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGlu 137
 DB 472 GAGTGAAGCAAAATGATCAGAGAAAGATATTGATGAGACGAGCATCAACTATGAA 531
 QY 138 GluPheAlaArgMetLeu 143
 DB 532 GAATTCGTACAGATGATG 549

RESULT 15
 E02315 E02315 654 bp RNA linear PAT 29-SEP-1997
 LOCUS DNA encoding calmodulin.
 DEFINITION E02315
 ACCESSION E02315
 VERSION E02315.1 GI:2170551
 KEYWORDS JP 1990092286-A/2.
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus.
 Rattus norvegicus.
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Ratus.

REFERENCE 1 (bases 1 to 654)
 AUTHORS Ozawa, T., Matsuki, S. and Nozawa, Y.
 TITLE PRODUCTION OF CALMODULIN
 JOURNAL Patent: JP 1990092286-A 2 03-APR-1990;
 KIRIN BREWERY CO LTD

COMMENT

OS Rat
 PN JP 1990092286-A/2
 PD 03-APR-1990
 PF 30-SEP-1988 JP 1988246239
 PI OZAWA TADASHI, MATSUKI SHIGERU, NOZAWA YOSHINORI PC
 C12N15/12,C07H21/04,C07K13/00,C12P21/02,C12P21/02,C12R1:19); CC
 strandedness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC *source: clone-PRCM1;
 CC Feature is identified by experimental;
 FH key Location/Qualifiers

FEATURES
 source 1.654
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 214 a 153 c 159 g 128 t

BASE COUNT 214 a 153 c 159 g 128 t
 ORIGIN

[illegible]

LOCUS	DEFINITION	RATCAMP	LOCUS	DEFINITION	RATCAMP
599 bp	linear	ROD 27-APR-1993	599 bp	linear	ROD 27-APR-1993
complete cds	clone pRCM79.		complete cds	clone pRCM79.	

VERSION	M16659.1	GI:203259
KEYWORDS	calmodulin.	
SOURCE	Rat (strain Sprague-Dawley) male brain,	cdna to mRNA, clone pRCM79,
ORGANISM	Rattus norvegicus	

REFERENCE
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 599)
Sherbany, A.A., Parent, A.S. and Brosius, J.

JOURNAL	DNA 6 (3), 267-272 (1987)
MEDLINE	87246077
PUBMED	2885164
FEATURES	Location/Qualifiers

```

/organism="Rattus norvegicus"
/db_xref="taxon:10116"
<!. .599
/product="calmodulin mRNA"
mRNA

```

```

/note="calmodulin"
/codon_start=1
/protein_id="AAA0864.1"
/db_xref="GI:203260"

```

BASE COUNT 158 a 140 c 176 g 125 t
ORIGIN 9 bp upstream of NcoI site
AAELRHWTNIGKELTDEVDENMREADIDSGOVNVEEPQMMTAK"

Alignment Scores:	
Pred. No.:	9,87e-23
Score:	384.50
Percent Similarity:	73.07%
Length:	599
Matches:	76
Conservation:	23

Best Local Similarity:	52.05%	Mismatches:	35
Query Match:	52.74%	Indels:	3
DB:	10	Gaps:	2

Oy 1 MetAlaGlyGluLeuThrProGluGluGluIuaGlnTyrLysLysAlaPheSerAlaVal 20
 ||||| :||||| |::: ||::::::::::|||
Dd 11 ATGGCTGCACCACTATCCAGACAGATTCGAGAGTTCAAGAACCCTTCTCCCTTT 70

Oy **21** AsPTrraspGlyAsnGlyThrTlleasnIaGlnGluLeuGlyAlaAlaleuysAlaThr **40**

||| ||||||:||||||| | :||||||| | :|||:

[illegible]

RESULT 13	
AY046946	
LOCUS	622 bp mRNA linear MAM 18-SEP-2001
DEFINITION	Ovis aries calmodulin 2 (CALM2) mRNA, complete cds.
ACCESSION	AY046946

VERSION	AY046946..1	GI:1566/248
KEYWORDS		
SOURCE	Ovis aries.	
ORGANISM	Ovis aries	
Substrate	Meat	
Method	Chromatography, Electrophoresis, Gel Electrophoresis, Immunoblotting, Northern Blotting, Southern Blotting, Western Blotting	

REFERENCE
AUTHORS

1 (bases 1 to 622)
Gillett, A.M., Wallace, M.T., and Hooper, S. B.
Bovidae; Caprinae; Ovis.
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Caprinae; Ovis.

JOURNAL
REFERENCE
AUTHORS

in fetal sheep
unpublished
2 (bases 1 to 622)
Gillett, A.M., Wallace, M.J., Gillespie, M.T. and Hooper, S.B.

JOURNAL Submitted (19-JUL-2001) Physiology Dept., Monash University,
Wellington Rd, Clayton, Vic 3800, Australia

FEATURES location/Qualifiers

SOURCE 1. .622

gene	/db_xref="taxon:9940"
gene	1. .622
CDS	/gene="CALM2"
	69. .518

```

/codon_start=1
/product="calmodulin 2"
/protein_id="AAL02363.1"
/db_xref="GI:15667249"

```

BASE COUNT	ORIGIN
206 a	93 c 161 g 162 t

Alignment Scores:	
Pred. No.:	1.03e-22
Score:	384.50
Percent Similarity:	73.07%
Length:	622
Matches:	76
Conservative:	32

```
Best Local Similarity: 52.05% Mismatches: 35
Query Match: 52.74% Indels: 3
DB: 4 Gaps: 2
```

```

QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
DB 121 GGTCAAAATCCACAGAGAAATGACGATGATGATCAACAGAGATGCTGATGGC 180
QY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
DB 181 AATGGCACTATCAGCTTCCCTGAATCTTAAACCATGATGCGCAGAAAATGAAGGACACA 240
QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
DB 241 GACAGGAGAGAAATCCCTGAGGCAATTCGAGTCTTTACAAAGATGCGCAATGCTTAT 300
QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnGluProLeuProGlnGlu 117
DB 301 ATCAGTGGCGGACAGTACCTGATGTTATGACAACTTAGAGAAAAGCTTAACAGATGAA 360
QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrglu 137
DB 361 GAAGTAGACAAATGATCAAGAGAGACAGACATGATGGGATGGGCAAGTCAACTATGAA 420
QY 138 GluPheAlaArgMetLeu 143
DB 421 GAATTCGTACAGATGATG 438

RESULT 10
AX396241 485 bp DNA 1linear PAT 18-MAY-2002
LOCUS AX396241
DEFINITION Sequence 456 from Patent WO0212328.
ACCESSION AX396241
VERSION AX396241.1 GI:21066988
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 King, G.E., Meagher, M.J., Xu, J. and Secrist, H.
AUTHORS Compositions and methods for the therapy and diagnosis of colon
TITLE Cancer
JOURNAL Patent: WO 0212328-A 456 14-FEB-2002;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1..485
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 168 a 69 c 130 g 118 t
ORIGIN
Alignment Scores:
Pred. No.: 7.9e-23 Length: 485
Score: 384.50 Matches: 76
Percent Similarity: 73.97% Conservative: 32
Best Local Similarity: 52.05% Mismatches: 35
Query Match: 52.74% Indels: 3
DB: 6 Gaps: 2

US-10-031-403-1 (1-146) x AX396241 (1-485)
QY 1 MetAlaGlyLeuLeuThrProGluGluAlaGlnTyrlsLysAlaPheSerAlaVal 20
DB 44 ATGGCTGACCACTGACGAGAGAGATGCGAATTCAGAAAGCTTTTTCACATTTT 103
QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
DB 104 GACAAAGATGCTGATGACATATACAAACAAAGAAATGGGAATCTGTAAAGATCTCTT 163
QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
DB 164 GGGCAGATCCACAGAGAGAGATGACAGACATGATTAATGAAGTAGATGCTGATGAT 223
QY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
DB 224 AATGGCACTATCAGCTTCCCTGAATCTTGAACATGATGCGAAGAAAATGAAGAGACACA 283

```

```

QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
DB 284 GACAGTCAACAAAGAAATTAAGAGACATTCCTGCTGTTTATTAAGATGCGCAT 343
QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnGluProLeuProGlnGlu 117
DB 344 ATTAGTCTGACAGAACTCCCATGTGATGACAAACCTTGAGAGAAAGTTAAACAGATGAA 403
QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrglu 137
DB 404 GAAGTTGATGAATGATGACAGAGAGAGATATGATGATGATGATCAAGTAACTATGAA 463
QY 138 GluPheAlaArgMetLeu 143
DB 464 GAGTTTGTACAAATGATG 481

RESULT 11
SYNARBCAL 595 bp mRNA 1linear SYN 27-APR-1993
LOCUS SYNARBCAL
DEFINITION A.punctulata synthetic calmodulin mRNA, complete cds.
ACCESSION J04729
VERSION J04729.1 GI:207976
KEYWORDS calmodulin.
SOURCE A.punctulata (adult), cDNA to mRNA, clone M3MP18.
ORGANISM artificial construct.
REFERENCE
1 (bases 1 to 595)
AUTHORS Persechini, A., Blumenthal, D.K., Jarrett, H.W., Klee, C.B., Hardy, D.O.
and Kreislinger, R.H.
TITLE The effects of deletions in the central helix of calmodulin on
JOURNAL enzyme activation and peptide binding
MEDLINE J. Biol. Chem. 264 (14), 8052-8058 (1989)
PUBMED 89255236
COMMENT D.A. entry and computer-readable sequence for [1] kindly provided
by A.J. Persechini, 11-FEB-1989.
FEATURES
source Location/Qualifiers
1..595
/organism="synthetic construct"
/db_xref="taxon:32630"
146..595
/notes="calmodulin"
/codon_start=1
/transl_table=11
/protein_id="AA02214.1"
/db_xref="GI:207976"
/translation="MADQLTEQIAEFKAFSLPDKDGGCTTTKELGVMSIGQNP
TEHELDMDINEVDADNGTIDPEFTLTKARKKDDTDEETREARFVFDKDGNGTIS
AAELRVMTNLEKLTDEEVDKIRADIDGGQVNEEFVQMTAK"
CDS
146..595
/notes="calmodulin"
BASE COUNT 172 a 142 c 164 g 117 t
ORIGIN
Alignment Scores:
Pred. No.: 9.8e-23 Length: 595
Score: 384.50 Matches: 76
Percent Similarity: 73.97% Conservative: 32
Best Local Similarity: 52.05% Mismatches: 35
Query Match: 52.74% Indels: 3
DB: 12 Gaps: 2

US-10-031-403-1 (1-146) x SYNARBCAL (1-595)
QY 1 MetAlaGlyLeuLeuThrProGluGluAlaGlnTyrlsLysAlaPheSerAlaVal 20
DB 146 ATGGCTGACCACTGACGAGAGAGATGCGAATTCAGAAAGCTTTCTCCCTGTC 205
QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
DB 206 GACAAAGAGCGGATGCGCAATCAACCAAGAGAGCTGGGACCGGTGATGATCTCTT 265
QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60

```

	RESULT 8
E09262	E09262
LOCUS	E09262
DEFINITION	cDNA encoding human calmodulin.
ACCESSION	E09262
VERSION	E09262.1 GI:22025888
KEYWORDS	JP 1995126297-A/1.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Kato,M., Tou,A. and Saeki,M. CALMODULIN-FUSED PROTEIN Patent: JP 1995126297-A 1 16-MAY-1995;
AUTHORS	TITLE
JOURNAL	SAGAMI CHEM RES CENTER
COMMENT	OS Homo sapiens (human) PN JP 1995126297-A/1 PD 16-MAY-1995 PF 05-NOV-1993 JP 1993299041 PI KATO MASASHI, TOU AKOU, SAEKI MIHORO PC C07K14/575,C07K12/22,C12N15/09,C12P21/02,C12Q1/44,(C12P21/02, PC C07K14/575,C07K12/22,C12N15/09,C12P21/02,C12Q1/44,(C12P21/02, PC C12R1/91); CC strandedness: Double; CC topology: Linear; CC hypothetical: No; CC anti-sense: No; FH key Location/Qualifiers FT source FT FT FT FT FT FT FT CDS FT FT FT FT FEATURES source location/Qualifiers 1..450 /organism='Homo sapiens' /db_xref='taxon:9606'
BASE COUNT	167 a 61 c 115 g 107 t
ORIGIN	
Alignment Scores:	
Pred. No.: 7.3e-23 Length: 450	
Score: 384.50 Matches: 76	
Percent Similarity: 73.97% Conservative: 32	
Best Local Similarity: 52.05% Mismatches: 35	
Query Match: 52.74% Indels: 3	
DB: Gaps: 2	
US-10-031-403-1 (1-146) x E09262 (1-450)	
OY 1 MetaLaGlyLeuThrProGlInGUAlaGlnTYrLYsAlaLheSerAlaval 20	
Db 1 ATGGCTGCACCACTGACTGAAGAGCGAGATTCGACAATTCAAGAAGCTTTTCTACTAATT 60	
OY 21 AsprThraSPGLyAsNGlYThrLLeasmaLagInGUleUGlYALalaLeuysLatmr 40	
Db 61 GACCAAGATGTGATGAAGAACTTAACAACAAGGAATTGGAACGTGAATGAGATCTTT 120	
OY 41 GlytAsanLenSerGIuaLagInLeuarfYLSauILeserGIuValaSpseraspGly 60	
Db 121 GGCGAGCATCCACAGAAAGCACAGATTACAGACATGATTAATAAGATGACATCTGATGCT 180	
OY 61 AspGlyGuILIEseRPheGlnGIuPhelEuTr--AlaAlaArGLysAlaArg----- 77	
Db 181 AATGCCAACAAATGATCTCCCTGATTTCTGCACAATGATGGCAAAGAAAATGAAGACACA 240	
OY 78 AlaGlyLeuGluAsPLeuGlnValAlaLphearGalApheAspGlnAspGlyaspGlyHis 97	
Db 241 GACACTGAAGAAGAAATTAAGAACCATTCCTGTGTGGATTAAGAGATGGCAATGGCTAT 300	

QY	98	11ethrvalasp3luleuabrgahglametalaglyleugylc1nproleuproglingu	117
Db	301	ATTGCTGCTGCAGCACTTCGATGTGATGACAAACCTTTGGAGAAAGTTAAACACATGAA	360
QY	118	gluleaspalamer1learglulualaspvalasp3lunaspsylaryvalasntyrclu	137
Db	361	GAAGGTGATGAAGATGATCAGGAGACAGATATTGATGGTGAATGTCAGTAACATATGAA	420
QY	138	glupheal1aargmetleu	143
Db	421	GAGTTTGTAACAATGATG	438
RESULT 9			
LOCUS	DUKCA	476 bp	linear VRT 30-JUL-1999
DEFINITION	Anas platyrhynchos mRNA for calmodulin, complete cds.		
ACCESSION	D83350		
VERSION	D83350.1	GI:1199918	
KEYWORDS	calmodulin.		
SOURCE	Anas platyrhynchos cDNA to mRNA, clone_11b.lambda ZAP II		
ORGANISM	clone: pDI-34.		
REFERENCE	Anas platyrhynchos		
AUTHORS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.		
TITLE	1 (sites)		
JOURNAL	Kimura, N., Kurosawa, N., Kondo, K. and Tsukada, Y.		
MEDLINE	Molecular cloning of the kainate-binding protein and calmodulin		
REFERENCE	genes which are induced by an imprinting stimulus in ducklings		
AUTHORS	Brain Res. Mol. Brain Res. 17 (3-4), 351-355 (1993)		
TITLE	93287810		
JOURNAL	2 (bases 1 to 476)		
MEDLINE	Kimura, N.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (05-FEB-1996) Naohito Kimura, Soka University, Dept. of		
TITLE	Bioengineering, Faculty of Engineering; 1-236 Tangicho, Hachioji,		
JOURNAL	Tokyo 192, Japan (E-mail: kimura@scc1.t.soka.ac.jp,		
FEATURES	Tel:0426-91-9442, Fax:0426-91-9312)		
SOURCE	Location/Qualifiers		
	1..476		
	/organism="Anas platyrhynchos"		
	/db_xref="taxon:8839"		
	/clone="pDI-34"		
	/clone_11b="lambda ZAP II"		
	1..450		
	/codon_start=1		
	/product="calmodulin"		
	/protein_id="BAI11896.1"		
	/db_xref="GI:1199919"		
	/translation="MADQLTEEOQIAEFKEAFSLPDKDGGTITTKELGTVARSIGQNP		
	TEAELODMINEVDADNGSTIDFPEFLFMKMKMDTSESEIERAFRFQDKGNGYSI		
	AAELRHVMTNGLNTEKLTDEVDENIRLEADIDGGQVNEEFQVMYTA"		
BASE COUNT	162 a	84 c	122 g
ORIGIN			108 t
Alignment Scores:			
Pred. No.:	7.75e-23	Length:	476
Score:	384.50	Matches:	76
Percent Similarity:	73.97%	Conservative:	32
Best Local Similarity:	52.05%	Mismatches:	35
Query Match:	52.74%	Indels:	3
DB:	5	Gaps:	2
US-10-031-403-1 (1-146) x DUKCA (1-476)			
QY	1	Metala1gyluleuThrProglu1uglu1a1ag1nTfYfLysAla1PheSerAla1aVal	20
Db	1	ATGGCTGATCACTGACGAGAACAGATTTGCTGAGTTTCAAGGAGCCTTTCCCTATT	60
QY	21	AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaIleuysAlaThr	40
Db	61	GACAGAGAGTGTGATGTACTATTCACAAACAAAGAACTGGGAACCTGCATGAGGTGCTTG	120

REFERENCE 1 (bases 1 to 447)
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 AUTHORS Ozawa, T., Matsuki, S. and Nozawa, Y.
 TITLE PRODUCTION OF CALMODULIN
 JOURNAL Patent: JP 1990092286-A 1 03-APR-1990;
 KIRIN BREWERY CO LTD
 COMMENT
 OS Rat
 PN JP 1990092286-A/1
 PD 03-APR-1990
 PF 30-SEP-1988 JP 1988246239
 PI OZAWA TADASHI, MATSUKI SHIGERU, NOZAWA YOSHINORI PC
 C12N15/12,C07H21/04,C07K13/00,C12P21/02,(C12P21/02,C12R1:19); CC
 strandedness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC *source: clone=PTCAL7;
 CC Feature is identified by experimental;
 FH Key Location/Qualifiers
 FT mat_peptide 1..447
 FT /product="calmodulin".

FEATURES
 source location/Qualifiers
 1..447
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 BASE COUNT 155 a 87 c 122 g 83 t
 ORIGIN

Alignment Scores:
 Pred. No.: 7.25e-23 Length: 447
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 6 Gaps: 2

US-10-031-403-1 (1-146) x E02314 (1-447)

QY 1 MetAlaGlyLysLeuThrProGluGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
 Db 1 ATGGCAGATCAATTAACAGAGAAAGATCGTGAATTCAAAGAGCTTTTCTCCCTATT 60
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 Db 61 GATTAAGATGGCGAGCGACCATCACAACAAGAGAGCTGGGACTGTCATCGCTCACTG 120
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 121 GGTGACAGAACCCACAGAGCTGTAATCTGACATGATCAACGAGGTGATGCCGACGG 180
 QY 61 AspGlyLysLeuSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 Db 181 AATGGACCCATGCTCCAGAGTCTCTGATGATGCTAGAAAATGAAGAAAGACACA 240
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgLapheAspGlnAspGlyAspGlyHis 97
 Db 241 GATAGCGAAGAAAGAAATCCCTGAGCGCATTCGAGTCTTGACAAGATGGCAATGCTTAC 300
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117
 Db 301 ATGAGTCCGCGACAGAACGCCACGTCATCAACAACCTCGGGGAAAGCTTAACAGATGAA 360
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAspTyrGlu 137
 Db 361 GAAGTACACCAATGATCAAGAGAGAGATATTGATGAGAGCGACAGGTCAACTATGAA 420
 QY 138 GluPheAlaArgMetLeu 143
 Db 421 GAATTCTGACAGATGATG 438

RESULT 7
 CHKCALMA 450 bp mRNA linear VRT 28-APR-1993
 LOCUS Chicken calmodulin mRNA, complete cds.
 DEFINITION M36167.1 GI:211385
 ACCESSION M36167.1
 VERSION 1
 KEYWORDS Chicken, cDNA to mRNA.
 SOURCE Gallus gallus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 450)
 AUTHORS Iida, Y.
 TITLE cDNA sequences and molecular evolution of calmodulin genes of
 chicken and eel
 JOURNAL Bull. Chem. Soc. Jpn. 57, 2667-2668 (1984)

FEATURES
 source location/Qualifiers
 1..450
 /organism="Gallus gallus"
 /db_xref="taxon:9031"
 1..450
 /note="calmodulin"
 /codon_start=1
 /protein_id="AA048650.1"
 /db_xref="GI:211386"
 /translation="MADQLTEQIAEFKFAFLDKDGDGTTTKELGVMSLGNP
 TEAELODMINEVDAGNGTIDPEFLTMARKKQTDSEIEIAREARVFDKNGYIS
 AAEIRHVMNIEKLIDEVDEIRADLDGQVYEEVQWMTAK"

BASE COUNT 160 a 62 c 122 g 106 t
 ORIGIN

Alignment Scores:
 Pred. No.: 7.3e-23 Length: 450
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 5 Gaps: 2

US-10-031-403-1 (1-146) x CHKCALMA (1-450)

QY 1 MetAlaGlyLysLeuThrProGluGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
 Db 1 ATGGCAGATCAATTAACAGAGAAAGATCGTGAATTCAAAGAGCTTTTCTCCCTATT 60
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 Db 61 GATTAAGATGGCGAGCGACCATCACAACAAGAGAGCTGGGACTGTCATCGCTCACTG 120
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 121 GGTGACAGAACCCACAGAGCTGTAATCTGACATGATCAATGAAAGATGCGATGAGC 180
 QY 61 AspGlyLysLeuSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 Db 181 AATGGACCAATGCTCCAGAGTCTCTGATGATGCTAGAAAATGAAGAAAGATACA 240
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgLapheAspGlnAspGlyAspGlyHis 97
 Db 241 GATAGCGAAGAAATTAAGAAAGCTTCGCTGTTTGACAAGATGGTAAATGCTTAC 300
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117
 Db 301 ATTAGTCTCGCAGAACTTCGTCATGATGATGACAAATCTTGGGGAGAGCTTAACAGATGAA 360
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAspTyrGlu 137
 Db 361 GAAGTATGATGAATGATTAAGAGAGAGATATTGATGATGATGATCAAGTAACTATGAA 420
 QY 138 GluPheAlaArgMetLeu 143
 Db 421 GAGTTTGTACAGATGATG 438

Best Local Similarity: 99.32% Mismatches: 0
 Query Match: 99.59% Indels: 0
 DB: 2 Gaps: 0

US-10-031-403-1 (1-146) x AL732437 (1-185926)

QY 1 Metlaigylguleuthrprogluglulaagntyrlyslasapheserlaval 20
 |||||||
 DB 90285 ATGGCCGGTAGCTGACCTCCGAGAGAGGCCAGTAACAAAGGCTTTCGCGCTT 90344
 |||||||

QY 21 Asphthraspglyasnaglthrileasnaglulgluaglyalaaleulysalathr 40
 |||||||
 DB 90345 GACACGGATGGAAACGGACCATCATGCCAGAGAGCTGGCGCGGCTTAAGGCCACG 90404
 |||||||

QY 41 Glylysnasnleuserglulaaglnleuarglyslleuilesergluvalaspsersapgly 60
 |||||||
 DB 90405 GGCAGAGAACCTCTCGAGGCGCCACACTAAGAACTCATCTCCGAGGTTGACAGCGAGCGC 90464
 |||||||

QY 61 Aspglyglulieserphneglnluphelnhrhlaalaarglyalaarglyleu 80
 |||||||
 DB 90465 GACGGCGAAATACACTTCACAGAGTTCCTGAGCGCGGAGGAGGCGCGCGCTG 90524
 |||||||

QY 81 Gluaspleuglnvalalapheargalaphespglnaspglyaspglyhisilthrval 100
 |||||||
 DB 90525 GAGGACCTGCGAGTCCGCTTCGCGCTTCGACAGATGCGGAGCGGCACATCACCTG 90584
 |||||||

QY 101 Aspgluleuarargalamelataglyleuglylnproleuproglnlgluleuasp 120
 |||||||
 DB 90585 GACAGAGCTCAGCGCGGCATGCGCGGCTGCGGCGCGGCGGAGGAGGAGCTGAC 90644
 |||||||

QY 121 Alamelilearaglnalaaasvalaspglnaspglyarvalasntyrlyglulphela 140
 |||||||
 DB 90645 GCCATGATCCGCGGCGGCGGAGCTGACAGGAGGCGGCTGAGACTACGAGAGCTGCG 90704
 |||||||

QY 141 Argmetleualaglnlu 146
 |||||||
 DB 90705 AGATGCTCGCCAGAG 90722
 |||||||

RESULT 5
 AC103443/c 106359 bp DNA linear HTG 12-JUL-2002
 LOCUS Rattus norvegicus clone CH230-178G9, *** SEQUENCING IN PROGRESS
 DEFINITION *** 57 unordered pieces.
 AC103443
 VERSION AC103443.3 GI:21728753
 KEYWORDS HTG, HTGS_PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 106359)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
 Barbieri,J., Benton,J., Blmage,K., Blankenburg,K., Bonini,D.,
 Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
 Bukey,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
 Carion,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
 Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
 Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
 Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
 Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
 Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
 Hernandez,O., Hodgson,A., Hognes,M., Hollaway,C., Hollins,B.,
 Homs,F., Howard,S., Huber,D., Huiyk,S., Hume,J., Jackson,L.E.,
 Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
 Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
 Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,

Li,J., Li,Z., Licharge,O., Lien,C., Liu,J., Liu,W., Loulseged,H.,
 Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
 Maheshwari,M., Mapa,P., Martin,R., Martindale,A., Martinez,E.,
 Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
 Miner,G., Miner,Z., Mitchell,T., Mohabate,K., Morgan,M., Morris,S.,
 Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
 Nguyen,N., Nickerson,E., Nwokkenwo,S., Ogund,M., Okunodu,G.,
 Oragunye,N., Oviold,R., Pace,A., Payton,B., Peery,J., Perez,L.,
 Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
 Rivas,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savary,G.,
 Scherer,S., Scott,G., Shen,H., Shoochitari,N., Sisson,I.,
 Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
 Sutton,A., Swalek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
 Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
 Usmani,K., Vasquez,L., Vera,Y., Villalob,D., Vinson,R., Wang,Q.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wellington,S.,
 Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstock,G. and Gibbs,R.

Direct Submission
 2 (bases 1 to 106359)
 Unpublished
 Worley,K.C.

REFERENCE
 TITLE
 AUTHORS
 JOURNAL

REFERENCE
 TITLE
 AUTHORS
 JOURNAL

COMMENT
 Direct Submission
 Submitted (12-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 11, 2002 this sequence version replaced gi:17973266.
 Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 Project Information
 Center project name: GHOK
 Center clone name: CH230-178G9
 Summary Statistics
 Sequencing vector: plasmid.
 Chemistry: Dye-terminator Big Dye 1008 of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 53847 bases at least Q40
 Consensus quality: 57227 bases at least Q30
 Consensus quality: 60201 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 NOTE: This is a 'working draft' sequence; it currently
 consists of 57 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 1137: contig of 1137 bp in length
 1138 1237: gap of unknown length
 1238 2403: contig of 1166 bp in length
 2404 2503: gap of unknown length
 2504 3742: contig of 1239 bp in length
 3743 3842: gap of unknown length
 3843 5050: contig of 1208 bp in length
 5051 5150: gap of unknown length
 5151 6764: contig of 1614 bp in length
 6765 6864: gap of unknown length
 6865 7882: contig of 1018 bp in length
 7883 7982: gap of unknown length
 7983 9222: contig of 1240 bp in length

Oy	141	ArgmetLeuAlaGlnGlu	146
Dd	534	AGGATGCTCGCCACGAGC	551
RESULT 3			
LOCUS	AX399961	913 bp	DNA linear PAT 06-JUN-2002
DEFINITION	Sequence 132 from Patent WO0218424.		
ACCESSION	AX399961		
VERSION	AX399961.1	GI:21336273	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euthetia; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 Tang,Y.T., Asundi,V., Zhou,P., Xue,A.J., Ren,F., Zhang,J., Wang,J.R., Zhao,Q.A., Wang,D., Liu,C., Drmanac,R.T. and Wehrman,T.		
JOURNAL	Nucleic acids and polypeptides		
FEATURES	Patent: WO 0218424-A 132 07-MAR-2002;		
Source	HYSEQ, INC. (US)		
CDS	Location/Qualifiers		
	1..913		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	162..602		
	/note="unnamed protein product"		
	/codon_start=1		
	/protein_id="CAD33405.1"		
	/db_xref="GI:21336274"		
	/translation="MAGELTPEEEAOYKKAFAVDTDNGTINAQELGAALKATGNKI-		
	SEADLRKLISEVSDSGEISFOEFLIAAKKARAGEDLYAFAPFQDDGHITVED		
	LRRMAGIGQLPQEELDAMIREADVODDGRVNVEEFFARMLAG"		
BASE COUNT	175 a 279 c 321 g 138 t		
ORIGIN			
Alignment Scores:			
Pred. NO.:	6.77e-50	Length:	913
Score:	726.00	Matches:	145
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.32%	Mismatches:	0
Query Match:	99.59%	Indels:	0
DB:	6	Gaps:	0
US-10-031-403-1 (1-146) x AX399961 (1-913)			
Oy	1	MetaLalGlyGluLeuThrProGluGluGluAlaGlnTYrLYsAlaPheserAlaVal	20
Dd	162	ATGGCGGTGAGCTCACTCCGTGAGAGAGAGGCCCGCATCAAAGAAGCGCTTCCTCCGCGGT	221
Oy	21	AspThrAspGlyAsnGlyThrTrlIeasnAlaGlnGluLeuGlyAlaAlaLeuLYsAlaThr	40
Dd	222	GACACGGATGGAAAGGACCATCATATCCCCAGAGCTGGGGCGCGCTGAAGGCCACG	281
Oy	41	GlyLYsAsnLeuSerGluAlaGlnLeuArGYsLeuLIeserGluValAspserAspGly	60
Dd	282	GGCAAGAACCTCTCGGAGGCCACAGTAGAACAATCATCTCGAGTTGACAGCGACGGC	341
Oy	61	AspGlyGluLIeserPhgGlnGluPhelLeuThralAlaArGLYSAlaArgLaGlyLeu	80
Dd	342	GACGGCGAAATCACGTTCCAGAGATTCTTGACGGGGGGAAGAACGCCAGGCGCCGCTG	401
Oy	81	GluAspLeuGlnValAlaPharGlaAlaPhaspsGlnAspGlyAspGlyHisIleThrVal	100
Dd	402	GAGGACTCGCAGAGTGCCTTCGCGCCTTCGACCACGAGATGGACGGCCACATCACCGTG	461
Oy	101	AspGluLeuArGYarGalaMetAlaGlyLeuGlnProLeuProGlnGluGluLeuAsp	120
Dd	462	GACGAGCTCAGAGCGGGCATGCGGGGCTGGGGGACGCCGCTGCCGACAGAGAGCTGGAC	521
Oy	121	AlaMetIleArGgluaLaspyAlaspGlnAspGlyArGvalAsnTYrGluGluPhela	140

```

Db      522  GCCATGATCCGCGAGCCGACGTGACCGACGAGCGGGGTGAACACTACGAGAGATTCCG 581
Ox      141  ArgMetLeuAlaIngInU 146
          |||||
Db      582  AGGATGCTCGCCCGACGAG 599
RESULT 4
AL732437      185926 bp   DNA      linear   HTG_16-AUG-2002
LOCUS DEFINITION Homo sapiens chromosome 10 clone RP11-116G8, *** SEQUENCING IN
ACCESSION AL732437
VERSION HTG_16-AUG-2002
KEYWORDS HTG, HTGS_PHASE1, HTGS_ACTIVETERIN, HTGS_DRAFT, HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
           (bases 1 to 185926)
REFERENCE Direct Submission
AUTHORS Submitted (15-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
TITLE Cambridgehire, CB10 1SA, UK. E-mail enquiries:
JOURNAL humary@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
          On Aug 19, 2002 this sequence version replaced gi:22204501.
COMMENT ----- Genome Center
          Center: Wellcome Trust Sanger Institute
          Center code: SC
          Web site: http://www.sanger.ac.uk
          Contact: humary@sanger.ac.uk
          ----- Project Information
          Center project name: BAl16G8
          ----- Summary Statistics
          Assembly program: XGAP4; Version 4.5
          Sequencing vector: plasmid; 108752; 100% of reads
          Chemistry: Dye-terminator; 100% of reads
          Consensus quality: 185460 bases at least Q40
          Consensus quality: 185618 bases at least Q30
          Consensus quality: 185788 bases at least Q20
          Insert size: 185826; sum-of-contigs
          Insert size: 180559; 9.4% error; agarose-1p
          Quality coverage: 13.28x in Q20 bases; sum-of-contigs quality
          coverage: 14.38x in Q20 bases; agarose-1p
          -----
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 2 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          * 1 183441: contig of 183441 bp in length
          * 183442 183541: gap of 100 bp
          * 183542 185926: contig of 2385 bp in length.
          Location/Qualifiers
            1. 185926
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /chromosome="10"
               /clone="RP11-116G8"
               /clone_1db="RPC1-11.1"
               1. 183441
                  /note="assembly_fragment:02942"
                  183542, 185926
                  /note="assembly_fragment:03322"
BASE COUNT 50686 a 41277 c 45610 g 48253 t 100 others
ORIGIN
Alignment Scores:
Pred. No.: 1.83e-47 Length: 185926
Scores: 726.00 Matches: 145
Percent Similarity: 100.00% Conservative: 1

```

AX077138 858 bp DNA linear PAT 22-FEB-2001
 LOCUS AX077138 Sequence 2 from Patent WO0107604.
 DEFINITION AX077138 GI:13121753
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 858)
 AUTHORS Mehul, B., Bernard, D., and Simonetti, L.
 TITLE Isolated peptide of the horny layer and use thereof
 JOURNAL Patent: WO 0107604-A 2 01-FEB-2001;
 L'OREAL (FR)
 FEATURES
 source location/Qualifiers
 1. 858
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 155 a 267 c 301 g 135 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.65e-50 Length: 858
 Score: 729.00 Matches: 146
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 gaps: 0
 US-10-031-403-1 (1-146) x AX077138 (1-858)
 QY 1 MetAlaGlyGluLeuThrProGluGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
 Db 114 ATGGCCGGTGGAGTGCCTGCTGAGAGAGAGCCAGTACAAAGGCTTCTCCGGCGTT 173
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaLeuLysAlaThr 40
 Db 174 GACACGGATGGAAAGCGCACCATCAATGCCAGAGCTGGCGCGGCTGTAAGCCAGC 233
 QY 41 GlyLysAsnLeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValAspSerAspGly 60
 Db 234 GGCAAGAACCTCTCGAGGGCCACCTAAGAACTCATCTCGAGTTGACAGGAGCGCC 293
 QY 61 AspGlyLysLeuSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
 Db 294 GACGGCAAAATCACCTTCACAGAGTCTCTGACGGCGGCAAGAGGCCAGCGCGCTG 353
 QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
 Db 354 GAGGACCTGCAGGTGCGCTTCGCGCTTCGACCAAGATGGCGAGCGCCACATCACCCTG 413
 QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluGluLeuAsp 120
 Db 414 GACAGAGCTCAGGGCGGCGCATGCGGGGTGGCGAGCGCGTCCGCGAGAGAGACTGGAC 473
 QY 121 AlaMetIleArgGlnAlaAspValAspGlnAspGlyArgValAsnTyrGluGluPheAla 140
 Db 474 GCCATGATCCCGGAGCGGCGAGCTGACAGAGCGGGGTGAACCTACGAGAGATTCGCG 533
 QY 141 ArgMetLeuAlaGlnGlu 146
 Db 534 AGGATGCTCCGCCAGAG 551
 RESULT 2
 AF172852 858 bp mRNA linear PRI 01-MAY-2000
 LOCUS AF172852 Homo sapiens calmodulin-like skin protein (CLSP) mRNA, complete
 DEFINITION
 CDS
 ACCESSION AF172852
 VERSION AF172852.1 GI:7673315
 KEYWORDS
 SOURCE Homo sapiens.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 858)
 AUTHORS Mehul, B., Bernard, D., Simonetti, L., Bernard, M.A. and Schmidt, R.
 TITLE Identification and cloning of a new calmodulin-like protein from human epidermis
 JOURNAL J. Biol. Chem. 275 (17), 12841-12847 (2000)
 MEDLINE 20239936
 PUBMED 10777582
 REFERENCE 2 (bases 1 to 858)
 AUTHORS Mehul, B., Bernard, D., Simonetti, L. and Schmidt, R.
 TITLE Direct Submission.
 JOURNAL Submitted (27-JUL-1999) Life Science Research, L'oreal, 90 rue du general Roquet, Clichy 92583, France
 FEATURES
 source location/Qualifiers
 1. 858
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_type="keratinocyte"
 /tissue_type="skin"
 1. 858
 /gene="CLSP"
 114. 554
 /gene="CLSP"
 /note="calcium binding protein"
 /codon_start=1
 /product="calmodulin-like skin protein"
 /protein_id="AF66821.1"
 /db_xref="GI:7673315"
 /translation="MAGELTPEEEDQYKFAVSVDVDGNTIAGELGAALAKATGNTL
 SEALRLISEVSDGDEISFLEFLTAARAGAGLEDOVARFARPDGSDGHITVDE
 LRRAMGLGPLOEELDMIRADVDODGRVNYEEFRLAOE"
 BASE COUNT 155 a 267 c 301 g 135 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.65e-50 Length: 858
 Score: 729.00 Matches: 146
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 gaps: 0
 US-10-031-403-1 (1-146) x AF172852 (1-858)
 QY 1 MetAlaGlyGluLeuThrProGluGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
 Db 114 ATGGCCGGTGGAGTGCCTGCTGAGAGAGAGCCAGTACAAAGGCTTCTCCGGCGTT 173
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaLeuLysAlaThr 40
 Db 174 GACACGGATGGAAAGCGCACCATCAATGCCAGAGCTGGCGCGGCTGTAAGCCAGC 233
 QY 41 GlyLysAsnLeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValAspSerAspGly 60
 Db 234 GGCAAGAACCTCTCGAGGGCCACCTAAGAACTCATCTCGAGTTGACAGGAGCGCC 293
 QY 61 AspGlyLysLeuSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
 Db 294 GACGGCAAAATCACCTTCACAGAGTCTCTGACGGCGGCAAGAGGCCAGCGCGCTG 353
 QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
 Db 354 GAGGACCTGCAGGTGCGCTTCGCGCTTCGACCAAGATGGCGAGCGCCACATCACCCTG 413
 QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluGluLeuAsp 120
 Db 414 GACAGAGCTCAGGGCGGCGCATGCGGGGTGGCGAGCGCGTCCGCGAGAGAGACTGGAC 473
 QY 121 AlaMetIleArgGlnAlaAspValAspGlnAspGlyArgValAsnTyrGluGluPheAla 140
 Db 474 GCCATGATCCCGGAGCGGCGAGCTGACAGAGCGGGGTGAACCTACGAGAGATTCGCG 533

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 16, 2003, 02:38:12 ; Search time 2428 Seconds

(without alignments)
1750.004 Million cell updates/sec

Title: US-10-031-403-1

Perfect score: 729

Sequence: 1 MAGELTPEEEAQQYKKAFAV.....DVDQDGRVNYEEFARMLAGE 146

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+g2n.model -DEV=x1h
-O=/cg2n.1/USPTC.spool/US10031403/runat_08052003.131924.5681/app_query.fasta.1.327
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR.SCORE=Pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10031403 @CGN.1.1.2466 @runat_08052003.131924.5681 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_WMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -IONLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: gb_da:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_of:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pin:*
35: em_hg_rod:*
36: em_hg_mam:*
37: em_hg_yrt:*
38: em_sy:*
39: em_hggo_hum:*
40: em_hggo_mus:*
41: em_hggo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	729	100.0	858	6	AX077138 Sequence
2	729	100.0	858	9	AF172852 Homo sapi
3	726	99.6	913	6	AX399961 Sequence
4	726	99.6	185926	2	AL732437 Homo sapi
5	388.5	53.3	106359	2	AC103443 Rattus no
6	384.5	52.7	447	6	E02314 DNA encodin
7	384.5	52.7	450	5	CHRCALMA
8	384.5	52.7	450	6	E09262
9	384.5	52.7	476	5	DURCA
10	384.5	52.7	485	6	AX396241 Sequence
11	384.5	52.7	595	12	SYNARBCAL
12	384.5	52.7	599	10	RATCAM
13	384.5	52.7	622	4	AY046946
14	384.5	52.7	654	6	AX401676
15	384.5	52.7	654	6	E02315
16	384.5	52.7	691	10	RSPRCM4
17	384.5	52.7	722	10	MUSCALMDA
18	384.5	52.7	750	5	XELCAM
19	384.5	52.7	799	9	HUMCALCBP
20	384.5	52.7	812	5	XELCAM
21	384.5	52.7	1037	9	BC008597
22	384.5	52.7	1044	10	MUSCAM
23	384.5	52.7	1058	9	BC000454
24	384.5	52.7	1084	10	RATCAM
25	384.5	52.7	1112	10	RATCAM
26	384.5	52.7	1126	9	HUMCAM
27	384.5	52.7	1128	9	HUMALDN
28	384.5	52.7	1131	6	A31920
29	384.5	52.7	1133	9	BC006464
30	384.5	52.7	1134	9	BC003354
31	384.5	52.7	1158	9	BC026055
32	384.5	52.7	1161	9	BC018677
33	384.5	52.7	1163	9	BC017385
34	384.5	52.7	1164	9	BC008437
35	384.5	52.7	1201	10	BC021347
36	384.5	52.7	1361	6	AX305360
37	384.5	52.7	1361	10	MMCALMOD
38	384.5	52.7	1446	10	RNRCLM
39	384.5	52.7	1571	9	BC011834
40	384.5	52.7	1644	5	AF085250
41	384.5	52.7	2175	9	HUMCAM
42	384.5	52.7	2190	9	BC005137
43	384.5	52.7	3513	10	AF178845
44	383.5	52.6	848	3	AB063181
45	382.5	52.5	450	5	ELCALMA

RESULT 1

ALIGNMENTS